

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 17:02:24 ; Search time 183 Seconds
(without alignments)
951.404 Million cell updates/sec

Title: US-10-633-894-6
Perfect score: 1776
Sequence: 1 MPCMPCALPTGGLPHQHT.....ALRHMVLECCGSAGKLAQI 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1767	99.5	340	Q6IEZ1	Q6iez1 homo sapien
2	1649	92.8	319	O2C3_HUMAN	Q8n628 homo sapien
3	1009	56.8	317	Q8VFB0	Q8vfh0 mus musculu
4	1008	56.8	312	Q7TQU4	Q7tqu4 mus musculu
5	990	55.7	350	Q6IF45	Q6if45 homo sapien
6	985	55.5	312	OL15_MOUSE	P23275 mus musculu
7	984.5	55.4	309	O2G3_HUMAN	Q8ngz4 homo sapien
8	983	55.3	312	Q8VFF0	Q8vff0 mus musculu
9	978	55.1	334	Q6IEZ0	Q6iez0 mus musculu
10	977	55.0	314	Q8VFG3	Q8vfg3 mus musculu
11	976	55.0	312	O2J1_HUMAN	Q9gzk6 homo sapien
12	975	54.9	317	O2G2_HUMAN	Q8ngz5 homo sapien
13	972	54.7	311	O2J3_HUMAN	O76001 homo sapien
14	971.5	54.7	308	Q7TQU2	Q7tqu2 mus musculu
15	971	54.7	312	O2B8_HUMAN	P59922 homo sapien
16	967.5	54.5	320	O2W1_HUMAN	Q9y3n9 homo sapien
17	967	54.4	318	Q8NHA6	Q8nha6 homo sapien
18	966	54.4	312	Q6IF18	Q6ifi8 homo sapien
19	963.5	54.3	308	Q8VG14	Q8vg14 mus musculu
20	958.5	54.0	309	Q7TQT0	Q7tgt0 mus musculu
21	958	53.9	312	O2J2_HUMAN	O76002 homo sapien
22	955	53.8	317	Q7TQT8	Q7tgt8 mus musculu
23	954	53.7	316	Q8VFG4	Q8vfg4 mus musculu
24	953	53.7	314	Q8VFG9	Q8vfg9 mus musculu
25	951	53.5	312	Q8VER2	Q8ver2 mus musculu
26	950	53.5	306	Q7TQU1	Q7tqu1 mus musculu
27	948	53.4	313	Q7TQU5	Q7tqu5 mus musculu
28	947	53.3	312	O2C1_HUMAN	Q95371 homo sapien
29	945	53.2	312	Q6IF55	Q6if55 homo sapien
30	943	53.1	310	Q6MFX7	Q6mfx7 rattus norv
31	941.5	53.0	309	Q7TQT1	Q7tgt1 mus musculu

32	940	52.9	313	2	Q8VFB2	Q8vfb2 mus musculu
33	939	52.9	312	2	Q6NTB3	Q6ntb3 homo sapien
34	937	52.8	327	2	Q7TRZ5	Q7trz5 mus musculu
35	936.5	52.7	311	2	Q8VGX0	Q8vgx0 mus musculu
36	936	52.7	315	2	Q8VGV6	Q8vgv6 mus musculu
37	935	52.6	310	2	Q8VFB2	Q8vfb2 mus musculu
38	935	52.6	312	2	Q8VFC2	Q8vfc2 mus musculu
39	934	52.6	313	2	Q63394	Q63394 rattus norv
40	930	52.4	310	2	Q7TRL4	Q7trl4 mus musculu
41	928	52.3	309	2	Q8VFG1	Q8vfg1 mus musculu
42	927	52.2	312	2	Q6MFX4	Q6mfx4 rattus norv
43	922	51.9	326	2	Q7TQU0	Q7tqu0 mus musculu
44	920.5	51.8	311	2	Q7TQT4	Q7tgt4 mus musculu
45	919	51.7	317	2	Q8VFC1	Q8vfc1 mus musculu

ALIGNMENTS

RESULT 1

Q6IEZ1					
ID	Q6IEZ1	PRELIMINARY;	PRT;	340 AA.	
AC	Q6IEZ1;				
DT	05-JUL-2004 (TrEMBLrel. 27, Created)				
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)				
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)				
DE	Olfactory receptor OR1-30.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	PubMed=14983052; DOI=10.1073/pnas.0307882100;				
RA	Malnic B., Godfrey P.A., Buck L.B.;				
RT	"The human olfactory receptor gene family.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 101:2584-2589(2004).				
CC	- - SUBCELLULAR LOCATION: Integral membrane protein (By similarity).				
CC	- - SIMILARITY: Belongs to family 1 of G-protein coupled receptors.				
CC	- - MISCELLANEOUS: The sequence shown here is derived from an				
CC	EMBL/GenBank/DBJ third party annotation (TPA) entry.				
DR	EMBL; BK004471; DAA04869.1; -.				
DR	GO; GO:0016021; C:integral to membrane; IEA.				
DR	GO; GO:0004984; F:olfactory receptor activity; IEA.				
DR	GO; GO:0004872; F:receptor activity; IEA.				
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.				
DR	InterPro; IPR000276; GPCR_Rhodpsn.				
DR	InterPro; IPR000725; Olfact_receptor.				
DR	Pfam; PF00001; 7tm1; 1.				
DR	PRINTS; PR00237; GPCR_RHODOPSN.				
DR	PRINTS; PR00245; OLFACTORYR.				
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.				
DR	PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.				
KW	G-protein coupled receptor; Receptor; Transmembrane.				
SQ	SEQUENCE 340 AA; 37459 MW; F5EDD366BD1E50FF CRC64;				

Query Match 99.5%; Score 1767; DB 2; Length 340;
Best Local Similarity 99.4%; Pred. No. 5.2e-125;
Matches 338; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MPCMPCALPTGGLPHQHTMEIANVSSPEVFLGLGFSARPSLETVLFIIVLSFYMVSI	60
Db	1	MPCMPCALPTGGLPHQHTMEIANVSSPEVFLGLGFSARPSLETVLFIIVLSFYMVSI	60
Qy	61	LGNGIILVSHTDVHLHTPMYFFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVV	120
Db	61	LGNGIILVSHTDVHLHTPMYFFFLANLPFLDMSFTTSIVPQLLANLWGPQKTSYGGCVV	120
Qy	121	QFYISHWLGAECVLLATMSYDRYAAICRPLHYTVIMHPQLCLGLALASWLGLTSMVG	180
Db	121	QFYISHWLGAECVLLATMSYDRYAAICRPLHYTVIMHPQLCLGLALASWLGLTSMVG	180
Qy	181	STLTMLPLCGNCCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFFVPLPLGLILVSYG	240

Db 181 STLTMLPLCGNCCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFLPLGLILVSYG 240
QY 241 HIARAVLKIRSAEGRKKAFTNCSSHVAVVSLFYGSIIFMYLQPAKSTSHQCKFIALPYT 300
Db 241 HIARAVLKIRSAEGRKKAFTNCSSHVAVVSLFYGSIIFMYLQPAKSTSHQCKFIALPYT 300
QY 301 VVTPALNPLIYTLRNTTEVKSALRHMVLENC CGSAGKLAQI 340
Db 301 VVTPALNPLIYTLRNTTEVKSALRHMVLENC CGSAGKLAQI 340

RESULT 2
O2C3 HUMAN STANDARD; PRT; 319 AA.
AC Q8N628; Q8NGW7;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Olfactory receptor 2C3.
GN Name=OR2C3; Synonyms=OR2C4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.,
RA "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes";
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Melanoma;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Putative odorant receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -!- DATABASE: NAME=Human Olfactory Receptor Data Explorerium
(HORDE);
CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbols&

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or send an email to license@isb-sib.ch).

DR EMBL; AB065649; BAC05875.1; ALT_INIT.
DR EMBL; BC030717; AAH30717.1; --

DR Genew; HGNC:15005; OR2C3.
DR InterPro; IPR000276; GPCR Rhodpsn.
DR InterPro; IPR000725; Olfact_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PRINTS; PR00245; OLFACTORYR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Multigene family; Olfaction;
KW Transmembrane.
FT DOMAIN 1 25 Extracellular (Potential).
FT TRANSMEM 26 49 1 (Potential).
FT DOMAIN 50 57 Cytoplasmic (Potential).
FT TRANSMEM 58 79 2 (Potential).
FT DOMAIN 80 100 Extracellular (Potential).
FT TRANSMEM 101 120 3 (Potential).
FT DOMAIN 121 139 Cytoplasmic (Potential).
FT TRANSMEM 140 158 4 (Potential).
FT DOMAIN 159 195 Extracellular (Potential).
FT TRANSMEM 196 219 5 (Potential).
FT DOMAIN 220 236 Cytoplasmic (Potential).
FT TRANSMEM 237 259 6 (Potential).
FT DOMAIN 260 272 Extracellular (Potential).
FT TRANSMEM 273 292 7 (Potential).
FT DOMAIN 293 319 Cytoplasmic (Potential).
FT DISULFID 97 189 By similarity.
FT CARBOHYD 5 5 N-linked (GlcNAc..) (Potential).
FT CONFLICT 19 19 A -> T (in Ref. 1).
FT CONFLICT 67 67 S -> P (in Ref. 1).
SQ SEQUENCE 319 AA; 35204 MW; C1433C539904DB19 CRC64;

Query Match 92.8%; Score 1649; DB 1; Length 319;
Best Local Similarity 100.0%; Pred. No. 3.7e-116;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 MEIANVSSPEVFLVLLGFSARPSLETVLFIVLSFYVMVSIILNGIILVSHSTDVHLHTPMY 81
Db 1 MEIANVSSPEVFLVLLGFSARPSLETVLFIVLSFYVMVSIILNGIILVSHSTDVHLHTPMY 60
QY 82 FFLANLSFLDMSFTTSIVPOLLANLWGPQKTSISYGGCVVQFYISHWLGATECVLLATMSY 141
Db 61 FFLANLSFLDMSFTTSIVPOLLANLWGPQKTSISYGGCVVQFYISHWLGATECVLLATMSY 120
QY 142 DRYAAICRPLHYTVMHPQLCLGLALASWLGGLTSMVSGTSLTMLLPLCGNCCIDHFFCE 201
Db 121 DRYAAICRPLHYTVMHPQLCLGLALASWLGGLTSMVSGTSLTMLLPLCGNCCIDHFFCE 180
QY 202 MPLIMQLACVDTSLNEMEMYLASFVFLVPLGLILVSYGHIAVAVLKIRSAEGRKKAFT 261
Db 181 MPLIMQLACVDTSLNEMEMYLASFVFLVPLGLILVSYGHIAVAVLKIRSAEGRKKAFT 240
QY 262 CSSHVAVVSLFYGSIIFMYLQPAKSTSHQCKFIALFYTVVTPALNPLIYTLRNTTEVKS 321
Db 241 CSSHVAVVSLFYGSIIFMYLQPAKSTSHQCKFIALFYTVVTPALNPLIYTLRNTTEVKS 300
QY 322 LRHMVLENC CGSAGKLAQI 340
Db 301 LRHMVLENC CGSAGKLAQI 319

RESULT 3
Q8VFH0
ID Q8VFH0 PRELIMINARY; PRT; 317 AA.
AC Q8VFH0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Olfactory receptor MOR256-12.
GN Name=Olf1361;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21676863; PubMed=11802173;
RA Zhang X., Firestein S.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 5:124-133(2002).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=21864068; PubMed=11875048; DOI=10.1093/hmg/11.5.535;
RX Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L.,
RA Trask B.J.;
RT "Different evolutionary processes shaped the mouse and human olfactory
receptor gene families.";
RL Hum. Mol. Genet. 11:535-546(2002).
[3]
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY073556; AAL61219.1; -.
DR MGD; MGI:3031195; Olfr1361.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004984; F:olfactory receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00245; OLFACTORYR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 317 AA; 35424 MW; 7DFOEF9EC7147B00 CRC64;

Query Match 56.8%; Score 1009; DB 2; Length 317;
Best Local Similarity 61.9%; Pred. No. 5.1e-68;
Matches 190; Conservative 51; Mismatches 64; Indels 2; Gaps 2;

QY 21 MMEIANVSSPEVFVLLGFSARPSLETVLFIVVLSFYMVSIILNGIILVSHTDVHLHTPM 80
Db 5 VMEKENTSSPEGFILVGFSDRPHLEILFVVLVSFYLLTLGNMTIILSALDSRLHTPM 64

QY 81 YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVVQFYISHWLGATECVLLATMS 140
Db 65 YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVVQFYISHWLGATECVLLAVMA 124

QY 141 YDRYAAICRPLHYTVIMHPQLCLGLALASWLGLTTSVMVGSTLTMLPLCGNNCIDHFFC 200
Db 125 YDRYAAVCKPLHYTVIMHPRLCGQLASVAWLSGFGNSLIMAPQTLMLPRCGHRRVDHFLC 184

QY 201 EMPLIMQLACVDT-SLNEMEMYLASFVVFVPLGLLILVSYGHIARAVLKIRSAEGRRKAF 259
Db 185 EMPALIGMACVDTMALALAFALAFI-ILAPLILILISYGIARAVFRIKSAAGRRAKAF 243

QY 260 NTCSSHVAVVSLFYGSIIFMYLQPAKSTSHQKGFIALFYTVVTPALNPLIYTLRNTEVK 319
Db 244 NTCSSHLIVVSLFYGTIIYMYLQPAPTYSDQGGKFLTLYFTIVTPSVNPLIYTLRNKDVK 303

QY 320 SALRHMV 326
Db 304 EAVKKVL 310

RESULT 4
Q7TQU4
ID Q7TQU4 PRELIMINARY; PRT; 312 AA.
AC Q7TQU4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26; Last annotation update)
DE Olfactory receptor Olfr1361.
GN Name=Olfr1361;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22974002; PubMed=14611657; DOI=10.1186/gb-2003-4-11-r71;
RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
RA Walker M., Williams E.M., Trask B.J.;
RT "Odorant receptor expressed sequence tags demonstrate olfactory
expression of over 400 genes, extensive alternate splicing and unequal
expression levels.";
RL Genome Biol. 4:R71-R71(2003).
[2]
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RA Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY318570; AAP71745.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 312 AA; 34766 MW; 79B51A4BF642716A CRC64;

Query Match 56.8%; Score 1008; DB 2; Length 312;
Best Local Similarity 62.1%; Pred. No. 6e-68;
Matches 190; Conservative 50; Mismatches 64; Indels 2; Gaps 2;

QY 22 MEIANVSSPEVFVLLGFSARPSLETVLFIVVLSFYMVSIILNGIILVSHTDVHLHTPMY 81
Db 1 MEKENTSSPEGFILVGFSDRPHLEILFVVLVSFYLLTLGNMTIILSALDSRLHTPMY 60

QY 82 FFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVVQFYISHWLGATECVLLATMSY 141
Db 61 FFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVVQFYISHWLGATECVLLAVMAY 120

QY 142 DRYAAICRPLHYTVIMHPQLCLGLALASWLGLTTSVMVGSTLTMLPLCGNNCIDHFFCE 201
Db 121 DRYAAVCKPLHYTVIMHPRLCGQLASVAWLSGFGNSLIMAPQTLMLPRCGHRRVDHFLCE 180

QY 202 MPLIMQLACVDT-SLNEMEMYLASFVVFVPLGLLILVSYGHIARAVLKIRSAEGRRKAFN 260
Db 181 MPALIGMACVDTMALALAFALAFI-ILAPLILILISYGIARAVFRIKSAAGRRAKFN 239

QY 261 TCSSHVAVVSLFYGSIIFMYLQPAKSTSHQKGFIALFYTVVTPALNPLIYTLRNTEVKS 320
Db 240 TCSSHLIVVSLFYGTIIYMYLQPAPTYSDQGGKFLTLYFTIVTPSVNPLIYTLRNKDVKE 299

QY 321 ALRHMV 326
Db 300 AVKKVL 305

RESULT 5
Q6IF45
ID Q6IF45 PRELIMINARY; PRT; 350 AA.
AC Q6IF45;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Olfactory receptor OR1-33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14983052; DOI=10.1073/pnas.0307882100;
RA Malnic B., Godfrey P.A., Buck L.B.;
RT "The human olfactory receptor gene family.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2584-2589(2004).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK004417; DAA04815.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004984; F:olfactory receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR000725; Olfact_receptor.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PRINTS; PR00245; OLFACTORYR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 350 AA; 38760 MW; 79D78A979DFD76CC CRC64;

Query Match 55.7%; Score 990; DB 2; Length 350;
Best Local Similarity 54.8%; Pred. No. 1.5e-66;
Matches 188; Conservative 63; Mismatches 68; Indels 24; Gaps 3;

QY 3 CMPC-----ALPTGGLPHPQHTMMEIANVSSPEVFLVLLGFSARPSLETVLFIIVLS 54
Db 24 CFGCTHSIPALGADPPGG-----MGLGNESLMDFILLGFSDDHPLEAVLFVFLF 74

QY 55 FYMVSIILNGIILVSHVTHDVLHTPMYFFLANLSFLDMSFTTSIVPQLLANLWGPQKTIS 114
Db 75 FYLLTLVGNFTIIISYLDPLPHTPMYFFLSNLLDICFTTSLAPQILVNLQRPKKTIT 134

QY 115 YGGCVVQFYISHWLGAECVILLATMSYDRAAICRPLHYTVIMHPQLCLGLALASWLGL 174
Db 135 YGGCVAQLYISLALGSTECILLADMALDRIYIAVCKPLHYVIMNPRLCQQLASISWLSGL 194

QY 175 TTSMVGSTLTMLPLCGNCCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFLPLGL 234
Db 195 ASSLIHATFTLQLPLCGNHRDLDFICEVPALLKLACVDTTVELVLFVVSFLVFIIPAL 254

QY 235 ILVSYGHIARAVLKIRSAEGRKAFNTCSSHVAVVSLFYGSIIFMYLQPAKSTSHEQKGF 294
Db 255 ISISYGFITQAVLRKISVEARHKAFSTCSSHLTVWIIIFYGTIIYVYLQPSDYSYADQKGF 314

QY 295 IALFYTVVTPALNPLIYTLRNTVEKVSALRHMVLENCSSAGKL 337
Db 315 ISLFYTMVTPTLNPIIYTLRNKOMKEALRKLL-----SGKL 350

RESULT 6
OL15_MOUSE STANDARD; PRT; 312 AA.
AC P23275;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Olfactory receptor 15 (OR3).
GN Name=Olf15;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93028384; PubMed=1384038;
RA Nef P., Hermans-Borgmeyer I., Artieres-Pin H., Beasley L.,
RA Dionne V.E., Heinemann S.F.;
RT "Spatial pattern of receptor expression in the olfactory epithelium.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:8948-8952(1992).
CC -!- FUNCTION: Putative odorant receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Olfactory epithelium.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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DR EMBL; M84005; AAA39862.1; -.
DR PIR; A46247; A46247.
DR MGD; MGI:106182; Olfr15.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR000725; Olfact_receptor.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PRINTS; PR00245; OLFACTORYR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Multigene family; Olfaction;
KW Transmembrane.
FT DOMAIN 1 24 Extracellular (Potential).
FT TRANSMEM 25 48 1 (Potential).
FT DOMAIN 49 57 Cytoplasmic (Potential).
FT TRANSMEM 58 79 2 (Potential).
FT DOMAIN 80 100 Extracellular (Potential).
FT TRANSMEM 101 120 3 (Potential).
FT DOMAIN 121 139 Cytoplasmic (Potential).
FT TRANSMEM 140 160 4 (Potential).
FT DOMAIN 161 200 Extracellular (Potential).
FT TRANSMEM 201 222 5 (Potential).
FT DOMAIN 223 236 Cytoplasmic (Potential).
FT TRANSMEM 237 261 6 (Potential).
FT DOMAIN 262 272 Extracellular (Potential).
FT TRANSMEM 273 292 7 (Potential).
FT DOMAIN 293 312 Cytoplasmic (Potential).
FT DISULFID 97 189 By similarity.
FT CARBOHYD 6 189 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 312 AA; 34333 MW; 8D3877EBBF51E132 CRC64;

Query Match 55.5%; Score 985; DB 1; Length 312;
Best Local Similarity 60.0%; Pred. No. 3.2e-66;
Matches 183; Conservative 50; Mismatches 72; Indels 0; Gaps 0;

QY 22 MEIANVSSPEVFLVLLGFSARPSLETVLFIIVLSFVMVSIILNGIILVSHVTHLTPMY 81
Db 1 MEVDSNSSSGTFLMGVSDHPHLEIIFFAVILASYLLTLVGNLTIIILSLRLDARLHTPMY 60

QY 82 FFLANLSFLDMSFTTSIVPQLLANLWGPQKTISYGGCVVQFYISHWLGAECVLLATMSY 141
Db 61 FFLSNLSSLDLAFTTSSVPQMLKNLWGPDKTISYGGCVTQLYVFLWLGATECILLVVMF 120

QY 142 DRYAAICRPLHYTVIMHPQLCLGLALASWLGLTSMVGSTLTMLPLCGNCCIDHFFCE 201
Db 121 DRYVAVCRPLHYTMNPRLCWGLAAISWLGGLGNSVIQSTFTLQLPFCGHRKVDNFLCE 180

QY 202 MPLIMQLACVDTSLNEMEMYLASFVFLVPLGLILVSYGHIARAVLKIRSAEGRKAFNT 261
Db 181 VPAMIKLACGDTSLNEAVLNGVCTFTTVPVSVILVSYCFIAQAVMKIRSVEGRRKAFNT 240

QY 262 CSSHVAVVSLFYGSIIFMYLQPAKSTSHQKGFIALFYTVVTPALNPLIYTLRNTVEKSA 321
Db 241 CVSHLVVVFLFYGSAIYGYLLPAKSSNQSGKGFISLFYSVTVPMNPLIYTLRNTVEKSA 300

QY 322 LRHMV 326
Db 301 LGRLL 305

RESULT 7
O2G3_HUMAN
ID O2G3_HUMAN STANDARD; PRT; 309 AA.
AC Q8NGZ4;
DT 10-OCT-2003 (Rel. 42, Created)

10-OCT-2003 (Rel. 42, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Olfactory receptor 2G3.
Name=OR2G3;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1] SEQUENCE FROM N.A.
Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
Tautsumi S., Aburatani H., Asai K., Akiyama Y.,
"Genome-wide discovery and analysis of human seven transmembrane helix
receptor genes."
Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
-|- FUNCTION: Putative odorant receptor.
-|- SUBCELLULAR LOCATION: Integral membrane protein.
-|- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
-|- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium
(HORDE);
WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbols&

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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).

EMBL; AB065622; BAC05848.1; -
Genew; HGNC:15008; OR2G3.
InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR000725; Olfact_receptor.
Pfam; PF00001; 7tm1; 1.
PRINTS; PR00237; GFCRRHODOPSN.
PRINTS; PR00245; OLFATORYR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Multigene family; Olfaction;
Transmembrane.
FT DOMAIN 1 25 Extracellular (Potential).
FT TRANSMEM 26 49 1 (Potential).
FT DOMAIN 50 57 Cytoplasmic (Potential).
FT TRANSMEM 58 79 2 (Potential).
FT DOMAIN 80 100 Extracellular (Potential).
FT TRANSMEM 101 120 3 (Potential).
FT DOMAIN 121 139 Cytoplasmic (Potential).
FT TRANSMEM 140 158 4 (Potential).
FT DOMAIN 159 195 Extracellular (Potential).
FT TRANSMEM 196 219 5 (Potential).
FT DOMAIN 220 236 Cytoplasmic (Potential).
FT TRANSMEM 237 259 6 (Potential).
FT DOMAIN 260 272 Extracellular (Potential).
FT TRANSMEM 273 292 7 (Potential).
FT DOMAIN 293 309 Cytoplasmic (Potential).
FT DISULFID 97 189 By similarity.
FT CARBOHYD 5 5 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 309 AA; 34506 MW; F72A80E3A753695C CRC64;
Query Match 55.4%; Score 984.5; DB 1; Length 309;
Best Local Similarity 57.6%; Pred. No. 3.5e-66;
Matches 182; Conservative 63; Mismatches 64; Indels 7; Gaps 1;
QY 22 MEIANVSSPEFVLGFSARPSLETVLFIIVLSFYMVSIILNGIILVSHTDVHLTPMY 81
Db 1 MGLGNESSLMDFILLGFSDPRLAEALVFVFFYLLTLVGNFTIIISYLDPLHTPMY 60
QY 82 FFLANLSFLDMSFTTSIVPQLLANLWGPQKTTISYGCVCVVQFYISHWLGATECVLLATMSY 141
Db 61 FFLSNLSLLDICFTTSLAPQTLVNLQRPKTTTYGGCVAQLYISLALGSTECILLADMAL 120
QY 142 DRYAAICRPLHYTVIMHPQLCLGLALASWLGLTTSVMVGSTLTMLLPLCGNNCIDHFFCE 201

Db 121 DRYIAVCKPLHYVVMNPRLCQQLASISWLSGLASSLIHATFTLQLPLCGNHRLDHFICE 180
QY 202 MPLIMQLACVDTSLNEMEMYLASFVVFVPLGLLILSVSYGHIAARAVLKIRSAEGRRKAFNT 261
Db 181 VPALLKLACVDTTVNELVLFVSVLVFVIPPALISISYGFITQAVLRIKSVEARHKAFST 240
QY 262 CSSHVAVVSFLFYGSIIIFYMLQPAKSTSHSQCKFIALFYTVVTPALNPLIYTLRNTVKSA 321
Db 241 CSSHLTVVIFIYGTIIYVYLQPSDSYAQDQGFISLFYTMVTPTLNPIIYTLRNKDMKEA 300
QY 322 LRHMVLENC CGSAGKL 337
Db 301 LRKLL-----SGKL 309
RESULT 8
Q8VFF0
ID Q8VFF0 PRELIMINARY; PRT; 312 AA.
AC Q8VFF0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Olfactory receptor MOR256-17 (Olfactory receptor Olfr15).
GN Name=Olfr15;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21676863; PubMed=11802173;
RA Zhang X., Firestein S.;
RT "The olfactory receptor gene superfamily of the mouse."
RL Nat. Neurosci. 5:124-133(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21864068; PubMed=11875048; DOI=10.1093/hmg/11.5.535;
RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L.,
RA Trask B.J.;
RT "Different evolutionary processes shaped the mouse and human olfactory
receptor gene families."
RL Hum. Mol. Genet. 11:535-546(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22974002; PubMed=14611657; DOI=10.1186/gb-2003-4-11-r71;
RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
RA Walker M., Williams E.M., Trask B.J.;
RT "Odorant receptor expressed sequence tags demonstrate olfactory
expression of over 400 genes, extensive alternate splicing and unequal
expression levels."
RL Genome Biol. 4:R71-R71(2003).
RN [5]
RP SEQUENCE FROM N.A.
RA Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AY073576; AAL61239.1; -
DR EMBL; AY317256; AAP70766.1; -
DR MGD; MGI:106182; Olfr15.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GFCRRHODOPSN.
DR PRINTS; PR00245; OLFATORYR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 312 AA; 34319 MW; DC7E30EBBD0750E9 CRC64;


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DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR00245; OLFACTORYR.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 314 AA; 35349 MW; E3C0069EA31011AB CRC64;

Query Match 55.0%; Score 977; DB 2; Length 314;
Best Local Similarity 57.0%; Pred. No. 1.3e-65;
Matches 174; Conservative 71; Mismatches 60; Indels 0; Gaps 0;

QY 22 MEIANVSSPEVFLGFSARPSLETVLFIIVLSFYMSILNGIILVSHLTDVHLHTPMY 81
Db 1 MEINKSSSETDFILLGFSRRPQLEHIISAVVEVFIIVTLVGNNTIILVSYLDSQLHTPMY 60

QY 82 FFLANLSFLDMSFTTSIVPQLLANLWGPQKTIISYGGCVVQFYISHWLGAECVLLATMSY 141
Db 61 FFLSNLSFVLDLCYTTISIVPQMLVNLWGPQKTIISYGGCVLQFFFDLGLGATECLLLAVMAY 120

QY 142 DRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVMGSTLTMLPLCGNCCIDHFFCE 201
Db 121 DRYAAVQCPLHYTVIMHPVLCQKWLASWLGGLSALILCSLTCLKPRCGHREVDFNFFCE 180

QY 202 MPLIMQLACVDTSLNEMEMYLASFVFFVVLPLGLILVSYGHIARAVLKIRSAEGRKAFNT 261
Db 181 MPALIKMACVYSRVIEIVFTLVGLVFLVPLSLILISYAVITQAVMKIKSATRWKVLNT 240

QY 262 CSSHVAVVSILFYGSIIFMYLQPAKSTSHQKFIALFYTVVTPALNPLIYTLRNTTEVKS 321
Db 241 CGSHLTVTTLFYGTLLIYMYMKPQNTISHQEQFTFTLYTIVTPSLNPLIYTLRNKDVKNA 300

QY 322 LRHMV 326
Db 301 VKRIIL 305

RESULT 11
O2J1_HUMAN STANDARD; PRT; 312 AA.
AC Q9GZK6; Q9GZK1;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Olfactory receptor 2J1 (Olfactory receptor 6-5) (OR6-5) (Hs6M1-4).
GN Name=OR2J1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT LEU-14.
RA Ziegler A., Ehlers A., Forbes S.A., Trowsdale J., Uchanska-Ziegler B.,
RA Volz A., Younger R., Beck S.;
RT "Polymorphic olfactory receptor genes and HLA loci constitute extended
RT haplotypes.";
RL (In) Kasahara M. (eds.);
RL Major histocompatibility complex-evolution, structure, and function,
RL pp.110-130, Springer-Verlag, Tokyo (2000).
CC -!- FUNCTION: Putative odorant receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -!- DATABASE: NAME=Human Olfactory Receptor Data Explorer
CC (HORDE);
CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbols";
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
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CC -----
DR EMBL; AJ302565; CAC20485.1; -.
DR EMBL; AJ302566; CAC20486.1; -.
DR EMBL; AJ302567; CAC20487.1; -.
DR EMBL; AJ302568; CAC20488.1; -.
DR EMBL; AJ302569; CAC20489.1; -.
DR EMBL; AJ302570; CAC20490.1; -.
DR Genew; HGNC:8259; OR2J1.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR000725; Olfact_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR00245; OLFACTORYR.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Multigene family; Olfaction;
KW Polymorphism; Transmembrane.
FT DOMAIN 1 26 Extracellular (Potential).
FT TRANSMEM 27 50 1 (Potential).
FT DOMAIN 51 58 Cytoplasmic (Potential).
FT TRANSMEM 59 80 2 (Potential).
FT DOMAIN 81 101 Extracellular (Potential).
FT TRANSMEM 102 121 3 (Potential).
FT DOMAIN 122 140 Cytoplasmic (Potential).
FT TRANSMEM 141 159 4 (Potential).
FT DOMAIN 160 196 Extracellular (Potential).
FT TRANSMEM 197 220 5 (Potential).
FT DOMAIN 221 237 Cytoplasmic (Potential).
FT TRANSMEM 238 260 6 (Potential).
FT DOMAIN 261 273 Extracellular (Potential).
FT TRANSMEM 274 293 7 (Potential).
FT DOMAIN 294 312 Cytoplasmic (Potential).
FT DISULFID 98 190 By similarity.
FT CARBOHYD 6 6 N-linked (GlcNAc..) (Potential).
FT VARIANT 14 14 I -> L.
FT SEQUENCE 312 AA; 35454 MW; 0C08C09B2D8A4835 CRC64;

Query Match 55.0%; Score 976; DB 1; Length 312;
Best Local Similarity 57.8%; Pred. No. 1.5e-65;
Matches 177; Conservative 54; Mismatches 75; Indels 0; Gaps 0;

QY 21 MMEIANVSSPEVFLGFSARPSLETVLFIIVLSFYMSILNGIILVSHLTDVHLHTPM 80
Db 1 MLMKKNASFEFFILLGFSNWPHEVVLFFVILIFYLITLIGNLFIILSYLDSHLHTPM 60

QY 81 YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTIISYGGCVVQFYISHWLGAECVLLATMS 140
Db 61 YFFLSNLSFLDLCYTTSSIPQLLVNLWGPQKTIISYAGCTVQLYFVLALGTAEVLLVMS 120

QY 141 YDYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVMGSTLTMLPLCGNCCIDHFFC 200
Db 121 YDYAAVQCPLHYTVIMHPRCRLLAASWVSGFTTSALHSSFTFWIPLCRHRLVDHFFC 180

QY 201 EMPLIMQLACVDTSLNEMEMYLASFVFFVVLPLGLILVSYGHIARAVLKIRSAEGRKAFN 260
Db 181 EVPALRLSCVDTQANELTLMVMSSIFVLIPLILITSYGAIRAVLSMQSTTGLQKVL 240

QY 261 TCSSHVAVVSILFYGSIIFMYLQPAKSTSHQKFIALFYTVVTPALNPLIYTLRNTTEVKS 320
Db 241 TCGAHLMVVSILFYFIPVCMYLPQPPSENQDQKFIALFYTVVTPSLNPLIYTLRNKDV 300

QY 321 ALRMV 326
Db 301 AVKRLM 306

..
RESULT 12
O2G2_HUMAN STANDARD; PRT; 317 AA.
ID -O2G2_HUMAN
AC Q8NGZ5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
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DR EMBL; AJ302554; CAC21442.1; --
DR EMBL; AJ302555; CAC21443.1; --
DR EMBL; AJ302556; CAC21444.1; --
DR EMBL; AJ302557; CAC20477.1; --
DR EMBL; AJ302558; CAC20478.1; --
DR EMBL; AF399630; AAK95115.1; --
DR Genew; HGNC:8261; OR2J3.
DR InterPro; IPR000276; GPCR Rhodpsn.
DR InterPro; IPR000725; Olfact_receptor.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00245; OLFACTORYR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Multigene family; Olfaction;
KW Polymorphism; Transmembrane.
FT DOMAIN 1 28 Extracellular (Potential).
FT TRANSMEM 29 52 1 (Potential).
FT DOMAIN 53 60 Cytoplasmic (Potential).
FT TRANSMEM 61 82 2 (Potential).
FT DOMAIN 83 103 Extracellular (Potential).
FT TRANSMEM 104 123 3 (Potential).
FT DOMAIN 124 142 Cytoplasmic (Potential).
FT TRANSMEM 143 161 4 (Potential).
FT DOMAIN 162 198 Extracellular (Potential).
FT TRANSMEM 199 222 5 (Potential).
FT DOMAIN 223 239 Cytoplasmic (Potential).
FT TRANSMEM 240 262 6 (Potential).
FT DOMAIN 263 275 Extracellular (Potential).
FT TRANSMEM 276 295 7 (Potential).
FT DOMAIN 296 311 Cytoplasmic (Potential).
FT DISULFID 100 192 By similarity.
FT CARBOHYD 8 8 N-linked (GlcNAc. .) (Potential).
FT VARIANT 113 113 T -> A (in allele 6M1-3*02).
FT VARIANT 226 226 R -> Q (in allele 6M1-3*02).
FT VARIANT 228 228 /FTID=VAR_010950.
FT VARIANT 261 261 /FTID=VAR_010951.
FT SEQUENCE 311 AA; 34950 MW; 84201145B9D5AA68 CRC64;
Query Match 54.7%; Score 972; DB 1; Length 311;
Best Local Similarity 58.1%; Pred. No. 3.1e-65;
Matches 175; Conservative 57; Mismatches 69; Indels 0; Gaps 0;
QY 26 NVSSPEVFLGFSARPSLETVLFIIVLSFYMVSIILGNGIILVSHTDVHLHTPMYFFLA 85
Db 8 NASSEGYFILVGFSNWPHEWIFVVLIFVYLMTLIGNLFIILSYLDSHLHTPMYFFLS 67
QY 86 NLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVVQFYISHWLGATECVLLATMSYDRIA 145
Db 68 NLSFLDLCYTTSSIPQLLVNLWGPEKTSYAGCMQLYFVLA LGTTTECVLLVVMYSYDRIA 127
QY 146 AICRPLHYTVIMHPQLCLGLALASWLGLTTSVMVGSITLMLPLCGNNCIDHFFCEMPLI 205
Db 128 AVCRLPHYTVLMHPRFCHLLAVASWVSGFTNSALHSSFTFWVPLCGHRQVDHFFCEVPAL 187
QY 206 MQLACVDTSLNEMEMYLASFVFLPLGLILVSYGHIARAVLKIRSAEGRRKAFNTCSSH 265
Db 188 LRLSCVDTHVNLTLMTSSIFVLIPLILITSYGAIVRAVLRMQSTGLQKVFGTGCAH 247
QY 266 VAVVSLFYGSIIFMYLQPAKSTSHQKGFIALFYTVVTPALNPLIYTLNTEVKSALRHM 325
Db 248 LMAVSLFFIPAMCIYLPSPSGNSQDQKGFIALFYTVVTPSLNPLIYTLRNKVVRGAVKRL 307
QY 326 V 326
Db 308 M 308

RESULT 14
Q7TQU2
ID Q7TQU2 PRELIMINARY; PRT; 308 AA.
AC Q7TQU2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Olfactory receptor Olfr1362.
GN Name=Olfr1362;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22974002; PubMed=14611657; DOI=10.1186/gb-2003-4-11-r71;
RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
RA Walker M., Williams E.M., Trask B.J.;
RT "Odorant receptor expressed sequence tags demonstrate olfactory
RT expression of over 400 genes, extensive alternate splicing and unequal
RT expression levels.";
RL Genome Biol. 4:R71-R71(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY318572; AAP71747.1; --
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 308 AA; 34477 MW; 5426728184F16EEF CRC64;
Query Match 54.7%; Score 971.5; DB 2; Length 308;
Best Local Similarity 60.5%; Pred. No. 3.3e-65;
Matches 188; Conservative 43; Mismatches 75; Indels 5; Gaps 1;
QY 22 MEIANVSSEVFLGFSARPSLETVLFIIVLSFYMVSIILGNGIILVSHTDVHLHTPMY 81
Db 1 MEKSNDSSEYGFILGFSRDRPRLEMLVFIIVNFTLYSVAVLGNITILVCILDPRLHTPMY 60
QY 82 FFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVVQFYISHWLGATECVLLATMSY 141
Db 61 FFLANLSFLDLCFSTCIPQMLVNLWGPDKTSYAGCVVQLFSFLSGSVEICILLAVMAY 120
QY 142 DRYAAICRPLHYTVIMHPQLCLGLALASWLGLTTSVMVGSITLMLPLCGNNCIDHFFCE 201
Db 121 DRYAAVCKPLHYMVIMHPQLCVRLMAVAVGWGLANAIIIMSPAMTLPGRGRRRINHFLCE 180
QY 202 MPLIMQLACVDTSLNEMEMYLASFVFLPLGLILVSYGHIARAVLKIRSAEGRRKAFNT 261
Db 181 MPALIKMACVDARPVEMLSFTLAILIIVLPLTLILVSYGYIAAAVLRKSAAGRWKAFNT 240
QY 262 CSSHVAVVSLFYGSIIFMYLQPAKSTSHQKGFIALFYTVVTPALNPLIYTLNTEVKS 321
Db 241 CSSHLTVVSLFYGSIIMYMQPGNSQDQKFLTLFYNLVTPLNPLIYTLRNKEMKGA 300
QY 322 LRHMVLENC 332
Db 301 LRKV-----CG 306
RESULT 15
O2B8 HUMAN
ID O2B8 HUMAN STANDARD; PRT; 312 AA.
AC P59922;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)

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OM protein - protein search, using sw model

Run on: April 8, 2005, 17:03:09 ; Search time 43 Seconds
(without alignments)
590.248 Million cell updates/sec

Title: US-10-633-894-6
Perfect score: 1776
Sequence: 1 MPCMPCALPTGGLLPHPQHT.....ALRHMVLENC CGSAGKLAQI 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep: *
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1776	100.0	340	US-09-546-986A-6	Sequence 6, Appli
2	1776	100.0	340	US-09-524-730-6	Sequence 6, Appli
3	977	55.0	334	US-09-546-986A-8	Sequence 8, Appli
4	977	55.0	334	US-09-524-730-8	Sequence 8, Appli
5	902	50.8	310	US-09-546-986A-2	Sequence 2, Appli
6	902	50.8	310	US-09-524-730-2	Sequence 2, Appli
7	823	46.3	331	US-09-546-986A-4	Sequence 4, Appli
8	823	46.3	331	US-09-524-730-4	Sequence 4, Appli
9	703	39.6	309	US-08-988-876-5	Sequence 5, Appli
10	674	38.0	316	US-08-827-291A-2	Sequence 2, Appli
11	672	37.8	314	US-08-988-876-7	Sequence 7, Appli
12	672	37.8	314	US-09-968-033C-5	Sequence 5, Appli
13	671.5	37.8	313	US-09-465-901-48	Sequence 48, Appl
14	669	37.7	321	US-08-748-506-10	Sequence 10, Appl
15	668	37.6	321	US-08-748-506-19	Sequence 19, Appl
16	667	37.6	321	US-08-748-506-11	Sequence 11, Appl
17	667	37.6	321	US-08-748-506-18	Sequence 18, Appl
18	653	36.8	321	US-08-748-506-12	Sequence 12, Appl
19	651	36.7	321	US-08-748-506-20	Sequence 20, Appl
20	648	36.5	321	US-08-748-506-13	Sequence 13, Appl
21	637.5	35.9	296	US-08-467-948A-2	Sequence 2, Appli
22	637.5	35.9	296	US-08-467-947A-2	Sequence 2, Appli
23	634	35.7	333	US-08-988-876-6	Sequence 6, Appli
24	609	34.3	284	1 US-08-118-270-61	Sequence 61, Appl
25	609	34.3	284	5 PCT-US93-08528-61	Sequence 61, Appl
26	596	33.6	277	1 US-08-118-270-62	Sequence 62, Appl
27	596	33.6	277	5 PCT-US93-08528-62	Sequence 62, Appl

28	576.5	32.5	284	1	US-08-118-270-67	Sequence 67, Appl
29	576.5	32.5	284	5	PCT-US93-08528-67	Sequence 67, Appl
30	564	31.8	247	1	US-08-465-980-3	Sequence 3, Appli
31	564	31.8	247	2	US-09-053-303-3	Sequence 3, Appli
32	564	31.8	247	3	US-09-339-115-3	Sequence 3, Appli
33	564	31.8	247	5	PCT-US95-07093-3	Sequence 3, Appli
34	561.5	31.6	274	1	US-08-118-270-69	Sequence 69, Appl
35	561.5	31.6	274	5	PCT-US93-08528-69	Sequence 69, Appl
36	555.5	31.3	269	1	US-08-118-270-64	Sequence 64, Appl
37	555.5	31.3	269	5	PCT-US93-08528-64	Sequence 64, Appl
38	543	30.6	327	3	US-08-748-506-14	Sequence 14, Appl
39	540	30.4	327	3	US-08-748-506-24	Sequence 24, Appl
40	537.5	30.3	293	1	US-08-118-270-60	Sequence 60, Appl
41	537.5	30.3	293	5	PCT-US93-08528-60	Sequence 60, Appl
42	537	30.2	327	3	US-08-748-506-22	Sequence 22, Appl
43	537	30.2	327	3	US-08-748-506-23	Sequence 23, Appl
44	535.5	30.2	286	1	US-08-118-270-65	Sequence 65, Appl
45	535.5	30.2	286	5	PCT-US93-08528-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1
US-09-546-986A-6
; Sequence 6, Application US/09546986A
; Patent No. 6635741
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Yang, Jianxin
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. 6635741el G-Protein Coupled Receptors
; FILE REFERENCE: 018781-004720US
; CURRENT APPLICATION NUMBER: US/09/546.986A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 09/524,730
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-546-986A-6

Query Match	100.0%;	Score 1776;	DB 4;	Length 340;
Best Local Similarity	100.0%;	Pred. No. 7.9e-149;		
Matches	340;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	MPCMPCALPTGGLLPHPQHTMMEIANVSSPEVFLVLLGFSARPSLETVLFIVVLSFYMVSI	60	
Db	1	MPCMPCALPTGGLLPHPQHTMMEIANVSSPEVFLVLLGFSARPSLETVLFIVVLSFYMVSI	60	
Qy	61	LNGIILVSHTDVHLHTPMYFFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCW	120	
Db	61	LNGIILVSHTDVHLHTPMYFFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCW	120	
Qy	121	QFYISHWLGATECVLLATMSYDHYAACRPLHYTVIMHPOLCLGLALASWLGGLTTSVMG	180	
Db	121	QFYISHWLGATECVLLATMSYDHYAACRPLHYTVIMHPOLCLGLALASWLGGLTTSVMG	180	
Qy	181	STLTMLPLCGNNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFFVPLGLLILVSYG	240	
Db	181	STLTMLPLCGNNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFFVPLGLLILVSYG	240	
Qy	241	HIARAVLKIRSAEGRRKAFNTCSSHVAVVSFLFYGSIIFMYLQPAKSTSHEQGFIALFYT	300	
Db	241	HIARAVLKIRSAEGRRKAFNTCSSHVAVVSFLFYGSIIFMYLQPAKSTSHEQGFIALFYT	300	
Qy	301	VVTPALNPLIYTLRNTTEVKSALRHMVLENC CGSAGKLAQI	340	
Db	301	VVTPALNPLIYTLRNTTEVKSALRHMVLENC CGSAGKLAQI	340	


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RESULT 2
US-09-524-730-6
; Sequence 6, Application US/09524730
; Patent No. 6638733
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Yang, Jianxin
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. 6638733el G-Protein Coupled Receptors
; FILE REFERENCE: 018781-004710US
; CURRENT APPLICATION NUMBER: US/09/524,730
; CURRENT FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-524-730-6

Query Match      100.0%; Score 1776; DB 4; Length 340;
Best Local Similarity 100.0%; Pred. No. 7.9e-149;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPCMPCALPTGGLPHQHTMMEIANVSSPEVFLGFSARPSLETVLFIVVLSFYMVSI 60
Db 1 MPCMPCALPTGGLPHQHTMMEIANVSSPEVFLGFSARPSLETVLFIVVLSFYMVSI 60

QY 61 LGNGIILVSHTDVHLHTPMYFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVV 120
Db 61 LGNGIILVSHTDVHLHTPMYFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVV 120

QY 121 QFYISHWLGATECVLLATMSYDYYAACRPLHYTVIMHPQLCLGLALASWLGLTTSVMG 180
Db 121 QFYISHWLGATECVLLATMSYDYYAACRPLHYTVIMHPQLCLGLALASWLGLTTSVMG 180

QY 181 STLTMLLPLCGNNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFFVPLPLGLILVSYG 240
Db 181 STLTMLLPLCGNNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFFVPLPLGLILVSYG 240

QY 241 HIARAVLKIRSAEGRKAFNTCSSHVAVVSLFYGSIIFMYLQPAKSTSHEQGKFIALFYT 300
Db 241 HIARAVLKIRSAEGRKAFNTCSSHVAVVSLFYGSIIFMYLQPAKSTSHEQGKFIALFYT 300

QY 301 VVTPALNPLIYTLRNTTEVKSALRHMVLENCGSAGKLAQI 340
Db 301 VVTPALNPLIYTLRNTTEVKSALRHMVLENCGSAGKLAQI 340

RESULT 3
US-09-546-986A-8
; Sequence 8, Application US/09546986A
; Patent No. 6635741
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Yang, Jianxin
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. 6635741el G-Protein Coupled Receptors
; FILE REFERENCE: 018781-004720US
; CURRENT APPLICATION NUMBER: US/09/546,986A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 09/524,730
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-546-986A-8

Query Match      55.0%; Score 977; DB 4; Length 334;
Best Local Similarity 58.5%; Pred. No. 2.3e-78;
Matches 183; Conservative 58; Mismatches 68; Indels 4; Gaps 1;

QY 18 QHT---MMEIANVSSPEVFLGFSARPSLETVLFIVVLSFYMVSIILVSHTD 73
Db 13 EHTLHGMVRHTNESNLGFIILGFSYAQLQKLVFLILILYLLTILGNTTILVSRLE 72

QY 74 VHLHTPMYFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVVQFYISHWLGATEC 133
Db 73 PKLHMPMYFFLSHLSELYRCFTSSVIPQLLVNLWEPMKTIAYGGCLVHLYNSHALGSTEC 132

QY 134 VLLATMSYDYYAACRPLHYTVIMHPQLCLGLALASWLGLTTSVMGSTLTMLPLCGNN 193
Db 133 VLPALMSCDRYVAVCRPLHYTVIMHILCMALASMAWLSGIATTLVQSTLTQLPFCGHR 192

QY 194 CIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFFVPLPLGLILVSYGHIAVARLKIRSAE 253
Db 193 QVDHFICEVPVLIKLACVGTTFNEAELFVASILFLIVPVSFILVSSGYIAHAVLRIKSAT 252

QY 254 GRRKAFNTCSSHVAVVSLFYGSIIFMYLQPAKSTSHEQGKFIALFYTVVTPALNPLIYTL 313
Db 253 GRQKAFGTCFSLTAVTIFYGTIIFMYLQPAKSSRDQKFSILFYTVVTRMLNPLIYTL 312

QY 314 RNTEVKSALRHMV 326
Db 313 RIKEVGALKKKVL 325

RESULT 4
US-09-524-730-8
; Sequence 8, Application US/09524730
; Patent No. 6638733
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Yang, Jianxin
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. 6638733el G-Protein Coupled Receptors
; FILE REFERENCE: 018781-004710US
; CURRENT APPLICATION NUMBER: US/09/524,730
; CURRENT FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-524-730-8

Query Match      55.0%; Score 977; DB 4; Length 334;
Best Local Similarity 58.5%; Pred. No. 2.3e-78;
Matches 183; Conservative 58; Mismatches 68; Indels 4; Gaps 1;

QY 18 QHT---MMEIANVSSPEVFLGFSARPSLETVLFIVVLSFYMVSIILVSHTD 73
Db 13 EHTLHGMVRHTNESNLGFIILGFSYAQLQKLVFLILILYLLTILGNTTILVSRLE 72

QY 74 VHLHTPMYFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVVQFYISHWLGATEC 133
Db 73 PKLHMPMYFFLSHLSELYRCFTSSVIPQLLVNLWEPMKTIAYGGCLVHLYNSHALGSTEC 132

QY 134 VLLATMSYDYYAACRPLHYTVIMHPQLCLGLALASWLGLTTSVMGSTLTMLPLCGNN 193
Db 133 VLPALMSCDRYVAVCRPLHYTVIMHILCMALASMAWLSGIATTLVQSTLTQLPFCGHR 192

QY 194 CIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFFVPLPLGLILVSYGHIAVARLKIRSAE 253
Db 193 QVDHFICEVPVLIKLACVGTTFNEAELFVASILFLIVPVSFILVSSGYIAHAVLRIKSAT 252

QY 254 GRRKAFNTCSSHVAVVSLFYGSIIFMYLQPAKSTSHEQGKFIALFYTVVTPALNPLIYTL 313
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Db 253 GRQAFGTCFSLTVVTIFYGTIIIFMYLQPAKSRSDQKFVSLFYVTVTRMLNPLIYTL 312
QY 314 RNTEVKSALRHMV 326
Db 313 RIKEVKGALKKVL 325

RESULT 5
US-09-546-986A-2
; Sequence 2, Application US/09546986A
; Patent No. 6635741
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Yang, Jianxin
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. 6635741el G-Protein Coupled Receptors
; FILE REFERENCE: 018781-004720US
; CURRENT APPLICATION NUMBER: US/09/546,986A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 09/524,730
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-546-986A-2

Query Match 50.8%; Score 902; DB 4; Length 310;
Best Local Similarity 54.2%; Pred. No. 8.8e-72;
Matches 166; Conservative 57; Mismatches 81; Indels 2; Gaps 1;
QY 29 SPEVFVLLGFSARPSLETVLFIIVLSFYMVSILGNGIILVSHTDVHLHTPMYFFLANLS 88
Db 5 SPKAFILLGVSDRPWLELPLFVVLVLLSYVLAMLGNAVAILASRVDPQLHSPMYIFLSHLS 64
QY 89 FLDMSTTSIVPQLLANLWGPQKTISYGGCVVQFYISHWLGATECVLLATMSYDRYAAIC 148
Db 65 FLDLCTTTTVPQMLVNMGSSQKTISYGGCTVQYAVFHWLGCTECIVLAAMALDRYVASC 124
QY 149 RPLHYTVIMHPQLCLGLALASWLGLTTSVMGSTLTMLPLCGNNCIDHFFCEMPLIMQL 208
Db 125 KPLHYAVLMHRALCQQLVALAWLSGFNSFVQVVLTVQLPFCGRQVLNPFCEVPAVIKL 184
QY 209 ACVDTSLNEMEMYLASFVVLPLGLILVSYGHIARAVLKIRSAEGRRKAFNTCSSHVAV 268
Db 185 SCADTAMNDTILAVLVAFFVLVPLALILLSYGFARAVLRIQSSKGRHKAFGTCSSHLMI 244
QY 269 VSLFYGSIIFMYLQPAKSTSHQCKFIALFYVTVTPALNPLIYTLRNTVEKVSALRHMV-- 326
Db 245 VSLFYLPALMYLQPPSSYSQEQGKFISLFYSIITPTLNPFYTLRNKMDKMGALRLLAR 304
QY 327 LENC CG 332
Db 305 IWRLCG 310

RESULT 6
US-09-524-730-2
; Sequence 2, Application US/09524730
; Patent No. 6638733
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Yang, Jianxin
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. 6638733el G-Protein Coupled Receptors
; FILE REFERENCE: 018781-004710US
; CURRENT APPLICATION NUMBER: US/09/524,730
; CURRENT FILING DATE: 2000-03-14

; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-524-730-2

Query Match 50.8%; Score 902; DB 4; Length 310;
Best Local Similarity 54.2%; Pred. No. 8.8e-72;
Matches 166; Conservative 57; Mismatches 81; Indels 2; Gaps 1;
QY 29 SPEVFVLLGFSARPSLETVLFIIVLSFYMVSILGNGIILVSHTDVHLHTPMYFFLANLS 88
Db 5 SPKAFILLGVSDRPWLELPLFVVLVLLSYVLAMLGNAVAILASRVDPQLHSPMYIFLSHLS 64
QY 89 FLDMSTTSIVPQLLANLWGPQKTISYGGCVVQFYISHWLGATECVLLATMSYDRYAAIC 148
Db 65 FLDLCTTTTVPQMLVNMGSSQKTISYGGCTVQYAVFHWLGCTECIVLAAMALDRYVASC 124
QY 149 RPLHYTVIMHPQLCLGLALASWLGLTTSVMGSTLTMLPLCGNNCIDHFFCEMPLIMQL 208
Db 125 KPLHYAVLMHRALCQQLVALAWLSGFNSFVQVVLTVQLPFCGRQVLNPFCEVPAVIKL 184
QY 209 ACVDTSLNEMEMYLASFVVLPLGLILVSYGHIARAVLKIRSAEGRRKAFNTCSSHVAV 268
Db 185 SCADTAMNDTILAVLVAFFVLVPLALILLSYGFARAVLRIQSSKGRHKAFGTCSSHLMI 244
QY 269 VSLFYGSIIFMYLQPAKSTSHQCKFIALFYVTVTPALNPLIYTLRNTVEKVSALRHMV-- 326
Db 245 VSLFYLPALMYLQPPSSYSQEQGKFISLFYSIITPTLNPFYTLRNKMDKMGALRLLAR 304
QY 327 LENC CG 332
Db 305 IWRLCG 310

RESULT 7
US-09-546-986A-4
; Sequence 4, Application US/09546986A
; Patent No. 6635741
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Yang, Jianxin
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. 6635741el G-Protein Coupled Receptors
; FILE REFERENCE: 018781-004720US
; CURRENT APPLICATION NUMBER: US/09/546,986A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 09/524,730
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-546-986A-4

Query Match 46.3%; Score 823; DB 4; Length 331;
Best Local Similarity 52.3%; Pred. No. 8.8e-65;
Matches 162; Conservative 47; Mismatches 83; Indels 18; Gaps 3;
QY 26 NVSSPEFVLLGFSARPSLETVLFIIVLSFYMVSILGNGIILVSHTDVHLHTPMYFFLA 85
Db 5 NASYLQAFILVGSDDRPGLEKILFAVILFICILTLVGNNTAIIILLVMDVRHLHTPMYFFLG 64
QY 86 NLSFLDMSFTTSIVPQLLANLWGPQKTISYGGCVVQFYISHWLGATECVLLATMSYDRYA 145
Db 65 NLSFLDLCTFASIAPQLLWNLGPEKTTIVHGCVAQLIYIMMLGSTECVLLVVMASHDRYV 124
QY 146 AICRPLHYTVIMHPQLCLGLALASWLGLTTSVMGSTLTMLPLCGNNCIDHFFCEMPLI 205

Db 125 AVCRSLHYMAVMRPHLCQLQVTVAWCCGFLNSFIMCPQTMQLSRCGRRVDHFLCEMPAL 184
QY 206 MQLACVDTSLNEMEMYLASFVFFVL-----PLGLILVS---YGHIAAVLKIRSAEGR 256
Db 185 IAMSCEETMLVEA-----IHLCPGGSPPGAALPHPHLYGVIAAAVLRMKSAAGR 235
QY 257 KAFNTCSSHVAVVSIFYGSIIFMYLQPAKSTSHQKGFIALFYVTVTPALNPLIYTLRNT 316
Db 236 KAFHTCSSHLTVVSLFYGTIIYVYLKPANSYSQDQKFLTFTYIVIPSINPLIYTLR 295
QY 317 EVKSALRHMV 326
Db 296 DVKGTMKKLL 305

RESULT 8
US-09-524-730-4
; Sequence 4, Application US/09524730
; Patent No. 6638733
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Yang, Jianxin
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. 6638733el G-Protein Coupled Receptors
; FILE REFERENCE: 018781-004710US
; CURRENT APPLICATION NUMBER: US/09/524,730
; CURRENT FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-524-730-4

Query Match 46.3%; Score 823; DB 4; Length 331;
Best Local Similarity 52.3%; Pred. No. 8.8e-65;
Matches 162; Conservative 47; Mismatches 83; Indels 18; Gaps 3;
QY 26 NVSSPEVFLVLLGFSARPSLETVLFIVVLSFYMVSIILNGNIIILVSHTDVHLHTPMYFFLA 85
Db 5 NASYLQAFILVGSDDRGLEKILFAVILIFCILTILVGNITAILLLVMDVRLHTPMYFFLG 64
QY 86 NLSFLDMSFTTSIVPQILLANLWGPQKTIISYGGCVVQFYISHWLGAECVLLATMSYDRYA 145
Db 65 NLSFLDLCFTASIAQQLLWNLGGPEKTIITHGCVAQLYIYMLGSTECVLLVVMVSHDRYV 124
QY 146 AICRPLHYTVIMHPQLCLGLALASWLGLTTSVMVGSTLTMLPLCGNNCIDHFFCEMPLI 205
Db 125 AVCRSLHYMAVMRPHLCQLQVTVAWCCGFLNSFIMCPQTMQLSRCGRRVDHFLCEMPAL 184
QY 206 MQLACVDTSLNEMEMYLASFVFFVL-----PLGLILVS---YGHIAAVLKIRSAEGR 256
Db 185 IAMSCEETMLVEA-----IHLCPGGSPPGAALPHPHLYGVIAAAVLRMKSAAGR 235
QY 257 KAFNTCSSHVAVVSIFYGSIIFMYLQPAKSTSHQKGFIALFYVTVTPALNPLIYTLRNT 316
Db 236 KAFHTCSSHLTVVSLFYGTIIYVYLKPANSYSQDQKFLTFTYIVIPSINPLIYTLR 295
QY 317 EVKSALRHMV 326
Db 296 DVKGTMKKLL 305

RESULT 9
US-08-988-876-5
; Sequence 5, Application US/08988876
; Patent No. 6063596
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Bandman, Olga

; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
; TITLE OF INVENTION: WITH IMMUNE RESPONSE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/988,876
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0441 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1314667
US-08-988-876-5

Query Match 39.6%; Score 703; DB 3; Length 309;
Best Local Similarity 46.5%; Pred. No. 3.1e-54;
Matches 140; Conservative 53; Mismatches 108; Indels 0; Gaps 0;
QY 22 MEIANVSSPEVFLVLLGFSARPSLETVLFIVVLSFYMVSIILNGNIIILVSHTDVHLHTPMY 81
Db 1 MELENDTRIPEFLLGLGFSEEPKLPFLFGLFSLMYLVTILGNLLILAVSSDSLHTPMY 60
QY 82 FFLANLSFLDMSFTTSIVPQILLANLWGPQKTIISYGGCVVQFYISHWLGAECVLLATMSY 141
Db 61 FFLANLSFVDICFTCTTIPKMLVNIQTKRVITYESCIIQMYFFELFAGIDNFLTVMAY 120
QY 142 DRYAAICRPLHYTVIMHPQLCLGLALASWLGLTTSVMVGSTLTMLPLCGNNCIDHFFCE 201
Db 121 DRYMAICYPLHYVMVIMNPQLCSLLLLVSWIMSALHSLQLTLMVLRSLPCTHFQIPHFFCE 180
QY 202 MPLIMQLACVDTSLNEMEMYLASFVFFVLPLGLILVSYGHIAAVLKIRSAEGRKAENT 261
Db 181 LNQMIQLACSDTFNNMMLYFAAILLGVAPLVGVLYSYFKIVSSIRGISAHSKYKAFST 240
QY 262 CSSHVAVVSIFYGSIIFMYLQPAKSTSHQKGFIALFYVTVTPALNPLIYTLRNTVKSA 321
Db 241 CASHLSVVSIFYCTSLGVYLSAAPQSTHSSVASVMYTVVTPMLNPFYISLRNKDIKGA 300
QY 322 L 322
Db 301 L 301
RESULT 10

US-08-827-291A-2
; Sequence 2, Application US/08827291A
; Patent No. 5874243
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Sathé, Ganesh
; TITLE OF INVENTION: NOVEL OLRCC15 RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,291A
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: GP50001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5015
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-827-291A-2

Query Match 38.0%; Score 674; DB 2; Length 316;
Best Local Similarity 43.3%; Pred. No. 1.2e-51;
Matches 125; Conservative 56; Mismatches 108; Indels 0; Gaps 0;
Qy 33 FVLLGFSARPSLETVLFIIVLSFYVMVSIILGNGIIILVSHTDVHLHTPMYFFLANLSFLDM 92
Db 12 FIFLGIFNHSPTHTLFFFLVLAIFSVAFMGNSVMVLLIYLDLTLHTPMYLLLSQLSLMDL 71
Qy 93 SFTTSIVPQLLANLWGPQKTIISYGGCVVQFYIISHWLGAECVLLATMSYDYYAAICRPLH 152
Db 72 MLICTTVPKMAFNVLSGSKSISMAGCATQIFFYTSLLGSECFLAVMAYDRYTAICHPLR 131
Qy 153 YTVIMHPQLCLGLALASWLGLTTSVMGSTLTMLLPLCGNNCIDHFFCEMPLIMQLACVD 212
Db 132 YTNLMSPKICGLMTAFSWILGSTDGIIVAVATFSFYCGSREIAHFFCELPSLLILSCND 191
Qy 213 TSLNEMEMYLASFVFFVPLPLGLILVSYGHIAARAVLKIRSAEGRRKAFNTCSSHVAVVSFL 272
Db 192 TSIFEKVIFICSIVMLVFPVAIIIASVAGVILAVIHMGSGEGRRKAFNTCSSHLMVVGME 251
Qy 273 YGSIIFMYLQPAKSTSHQKFIALFYTVVTPALNPLIYTLRNTVEKSA 321
Db 252 YGAGLFMYIQTSRDSPTQDKLVSVFYTLTPLNPLIYSLRNKEVTRA 300

RESULT 11
US-08-988-876-7
; Sequence 7, Application US/08988876
; Patent No. 6063596

; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
; TITLE OF INVENTION: WITH IMMUNE RESPONSE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/988,876
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0441 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 32086
; US-08-988-876-7

Query Match 37.8%; Score 672; DB 3; Length 314;
Best Local Similarity 43.9%; Pred. No. 1.7e-51;
Matches 133; Conservative 62; Mismatches 104; Indels 4; Gaps 2;
Qy 26 NVSSPEVFVLLGFSARPSLETVLFIIVLSFYVMVSIILGNGIIILVSHTDVHLHTPMYFFLA 85
Db 5 NQTSISDFLLGLPIQPEQQNLCYALFLAMYLTTLLGNLLIIVLRLDLSHLHTPMYLFLS 64
Qy 86 NLSFLDMSFTTSIVPQLLANLWGPQKTIISYGGCVVQFYIISHWLGAECVLLATMSYDYYA 145
Db 65 NLSFSDLCFSSVTIPKLLQNMNQDPSIPYADCLTQMYFFLLFGDLESLLVAMAYDRYV 124
Qy 146 AICRPLHYTVIMHPQLCLGLALASWLGLTT--SMVGSTLTMLLPLCGNNCIDHFFCEMP 203
Db 125 AICFPLHYTAIMSPMLCLALVALSV--LTFHAMLHTLLMARLFCFCADNVIPHFFCDMS 182
Qy 204 LIMQLACVDTSLNEMEMYLASFVFFVPLPLGLILVSYGHIAARAVLKIRSAEGRRKAFNTCS 263
Db 183 ALLKLAFTDRVNEWVIFIMGGLILVIPFLLILGSYARIVSSILKVFSSKGICKAFSTCG 242
Qy 264 SHVAVVSLFYGSIIFMYLQPAKSTSHQKFIALFYTVVTPALNPLIYTLRNTVEKSA 323
Db 243 SHLSVVSFLFYGTIVGLYLCSSANSSTLKDVTVMAMMYTVVTPMLNPFYSLNRDRMKGALS 302
Qy 324 HMV 326
Db 303 RVI 305

; LENGTH: 321 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-748-506-10

Query Match 37.7%; Score 669; DB 3; Length 321;
Best Local Similarity 47.1%; Pred. NO. 3.3e-51;
Matches 137; Conservative 46; Mismatches 108; Indels 0; Gaps 0;

Qy 33 FVLLGFSARPSLETVLFIVVLSFYMVSIILNGIILVSHWLGATECVLLATMSYDRYA 92
Db 18 FAFKFSEVPGECFLFNLLMLFLVSLTGNTLIVLAICTSPSLHTPMYFELANLSLLEI 77

Qy 93 SFTTSIVPQLLANLWGPQKTIISYGGCVVQFYISHWLGATECVLLATMSYDRYAAICRPLH 152
Db 78 GYTCSVIPKMLQSLVSEAREISREGCATQMFFAFFGITECCLLAAMAFDRCAICSPLH 137

Qy 153 YTVIMHPQCLGLALASWLGGLTTSVMGSTLTMLPLCGNNCIDHFFCEMPLIMQLACVD 212
Db 138 YATRMSREVCAHLAIVSWGMCIVSLGQTNFISLFCGPEIDHFFCDLPPLLALACGD 197

Qy 213 TSLNEMEMYLASFVVVPLPLGLILVSYGHIARAVLKIRSAEGRRKAFNTCSSHVAVVSLF 272
Db 198 TSQNEAAIFVVAVLICISSPFLLIISYVKILIAVLLMPSPEGRHKALSTCSSHLLVVTLF 257

Qy 273 YGSIIFMYLQPAKSTSHEQGFIALFYTVVTPALNPLIYTLRNTVEVKSALR 323
Db 258 YGSACITYLRPKSSHSPGMDKFLALFYTVVTSMLNPPIIYSLRNKEVKAALR 308

RESULT 15

US-08-748-506-19
; Sequence 19, Application US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Ronnett et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5600
; TELEFAX: 312-616-5700
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-748-506-19

Query Match 37.6%; Score 668; DB 3; Length 321;
Best Local Similarity 46.0%; Pred. NO. 4e-51;
Matches 137; Conservative 49; Mismatches 112; Indels 0; Gaps 0;

Qy 26 NVSSPEVFLVLLGFSARPSLETVLFIVVLSFYMVSIILNGIILVSHWLGATECVLLATMSYDRYA 85
Db 11 NSLSVKRFAFAKFPSEVPGECLLFTLLILMLFLVSLTGNALIALAACTSPSLHTPMYFFLA 70

Qy 86 NLSFLDMSFTTSIVPQLLANLWGPQKTIISYGGCVVQFYISHWLGATECVLLATMSYDRYA 145
Db 71 NLSLLEIGYTCVIPKMLQSLVSEAREISREGCATQMFFFGITECCLLAAMAFDRCM 130

Qy 146 AICRPLHYTVIMHPQCLGLALASWLGGLTTSVMGSTLTMLPLCGNNCIDHFFCEMPLI 205
Db 131 GICSPLHYATRMSREVCAHLAIVSWGMCIVGLGQTNNIISLFCGPEIDHFFCDLPPPL 190

Qy 206 MQLACVDTSLNEMEMYLASFVVVPLPLGLILVSYGHIARAVLKIRSAEGRRKAFNTCSSH 265
Db 191 LALACGDTSQNEAAIFVAAILCISPPFLVILYSYVRILVAVLVMPSPPEGRHKALSTCSSH 250

Qy 266 VAVVSLFYGSIIFMYLQPAKSTSHEQGFIALFYTVVTPALNPLIYTLRNTVEVKSALR 323
Db 251 LLVVTLFYGSVFTYLRPKSSHSPGMDKLLALFYTAVTSMNLNPPIIYSLRNKEVKAALR 308

Search completed: April 8, 2005, 17:13:16
Job time : 45 secs

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OM protein - protein search, using sw model

Run on: April 8, 2005, 16:53:23 ; Search time 173 Seconds
(without alignments)
760.107 Million cell updates/sec

Title: US-10-633-894-6
Perfect score: 1776
Sequence: 1 MPCMPICALPTGGLLPHPQHT.....ALRHMVLENCESAGKLAQI 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1776	100.0	340	4	AAG67467 Breast am
2	1776	100.0	340	6	ABR63705 Human G-p
3	1767	99.5	340	4	AAU24748 Human olf
4	1767	99.5	340	5	AAU85368 G-coupled
5	1755	98.8	337	6	ABR63707 Human G-p
6	1725	97.1	377	5	ABP95893 Human GPC
7	1654	93.1	320	6	ABR63708 Human G-p
8	1651	93.0	320	5	ABG66931 Novel G-p
9	1649	92.8	319	6	ABR63709 Human G-p
10	1646	92.7	320	5	ABJ04731 GPCR 11 p
11	1645	92.6	320	7	ADC86041 Human GPC
12	1641	92.4	319	4	AAG71912 Human olf
13	1641	92.4	319	4	AAG71896 Human olf
14	1640	92.3	319	6	ABU11186 Human G-p
15	1617	91.0	314	5	ABG76850 Human G-p
16	1565	88.1	305	5	ABJ04026 Human G-p
17	1565	88.1	305	8	ADH30926 Human G-p
18	990	55.7	350	4	AAU24714 Human olf
19	990	55.7	350	5	ABP95880 Human GPC
20	990	55.7	350	5	AAU85334 G-coupled
21	989	55.7	315	5	AAE18279 Human G-p
22	985	55.5	312	4	AAG72908 Human olf
23	985	55.5	312	4	AAG73035 Olfactory
24	985	55.5	312	8	ADH42027 Novel hum
25	985	55.5	334	5	ABB81444 Human GPC

26	984.5	55.4	309	4	AAG71891	Aag71891 Human olf
27	984.5	55.4	309	5	AAB71353	Aab71353 Human GCR
28	984.5	55.4	309	5	AAE18266	Aae18266 Human G-p
29	984.5	55.4	309	5	AAU95676	Aau95676 Human olf
30	984.5	55.4	309	5	ABB81445	Abb81445 Human GPC
31	984.5	55.4	309	7	ADC85565	Adc85565 Human GPC
32	984.5	55.4	309	7	ADJ83120	Adj83120 Human pro
33	984.5	55.4	314	6	ABR01597	Abro1597 Human G p
34	984	55.4	312	4	AAE10685	Aae10685 G-protein
35	984	55.4	312	8	ADH42039	Adh42039 Novel hum
36	984	55.4	312	8	ADH42041	Adh42041 Novel hum
37	984	55.4	334	4	AAU24698	Aau24698 Human olf
38	984	55.4	334	5	AAU85318	Aau85318 G-coupled
39	982	55.3	315	5	AAE18276	Aae18276 Human G-p
40	981	55.2	315	5	AAE18268	Aae18268 Human G-p
41	981	55.2	315	5	AAE18277	Aae18277 Human G-p
42	980	55.2	334	4	AAG72062	Aag72062 Human olf
43	979	55.1	311	8	ADH42037	Adh42037 Novel hum
44	979	55.1	311	8	ADH42047	Adh42047 Novel hum
45	979	55.1	315	5	AAE18275	Aae18275 Human G-p

ALIGNMENTS

RESULT 1
AAG67467
ID AAG67467 standard; protein; 340 AA.
XX AC AAG67467;
XX AC
DT 26-NOV-2001 (first entry)
XX
DE Breast amplified G protein coupled receptor (BCA-GPCR)-3.
XX
KW Breast amplified G protein coupled receptor; breast cancer;
KW chromosome 1q44; BCA-GPCR-1; BCA-GPCR-2; BCA-GPCR-3; BCA-GPCR-4;
KW signal transduction.
XX
OS Homo sapiens.
XX
PN WO200168704-A2.
XX PD
XX 20-SEP-2001.
XX PF 13-MAR-2001; 2001WO-US008020.
XX PR 14-MAR-2000; 2000US-00524730.
PR 11-APR-2000; 2000US-00546986.
XX (TULA-) TULARIK INC.
PA (POWE/) POWERS S.
PA (YANG/) YANG J.
PA (CUTL/) CUTLER G.
XX
PI Powers S, Yang J, Cutler G;
XX
DR WPI; 2001-570865/64.
DR N-PSDB; AAH78085.
XX
PT Four nucleic acids encoding breast amplified G protein coupled receptors
(BCA-GPCRs), useful for identifying modulators of G-protein coupled
PT receptor signal transduction which can be used in the treatment of cancer
PT such as breast cancer.
XX
PS Claim 14; Page 67-68; 68pp; English.
XX
CC The present sequence represents breast amplified G protein coupled
CC receptor (BCA-GPCR)-3. BCA-GPCRs are amplified and/or overexpressed in
CC breast cancer cells. The BCA-GPCRs are located at chromosome 1q44, in the
CC following orientation (starting from the centromere end): BCA-GPCR-1 (3'-
CC 5' orientation), BCA-GPCR-2 (5'-3' orientation), BCA-GPCR-3 (3'-5'
CC orientation), and BCA-GPCR-4 (5'-3' orientation). The G protein coupled

receptors are useful for assaying and identifying modulators of G-protein coupled receptor signal transduction. The modulators and antibodies against the G protein coupled receptors are useful for pharmacological modulation of signalling pathways, e.g. in cancer cells such as breast cancer

CC novel human G-protein coupled receptors (GPCR) which are amplified in
CC breast cancers. The sequences are useful in the treatment of cancers,
CC including breast and prostate cancers. The present sequence is a GPCR of
CC the invention


```
OS Homo sapiens.
XX WO2003054542-A1.
XX 03-JUL-2003.
XX 18-DEC-2002; 2002WO-US041112.
XX 20-DEC-2001; 2001US-00028521.
XX (TULA-) TULARIK INC.
XX Powers S, Yang J, Cutler G;
XX WPI; 2003-569288/53.
XX N-PSDB; ACC85515.
XX New G-protein coupled receptor (GPCR) polypeptides and nucleic acids,
XX useful for treating cancer, e.g. breast or prostate cancer.
XX Claim 10; Page 64; 77pp; English.
XX The present invention provides the protein and coding sequences of four
XX novel human G-protein coupled receptors (GPCR) which are amplified in
XX breast cancers. The sequences are useful in the treatment of cancers,
XX including breast and prostate cancers. The present sequence is a GPCR of
XX the invention
XX Sequence 337 AA;
Query Match 98.8%; Score 1755; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 5.3e-185;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 MPCALPTGGLLPHPQHTMMEIANVSSPEVFLVLLGFSARPSLETVLFIVVLSFYMVSILGN 63
Db 1 MPCALPTGGLLPHPQHTMMEIANVSSPEVFLVLLGFSARPSLETVLFIVVLSFYMVSILGN 60
QY 64 GIILVSHTDVLHHTPMYFFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSISYGGCVVQFY 123
Db 61 GIILVSHTDVLHHTPMYFFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSISYGGCVVQFY 120
QY 124 ISHWLGATECVLLATMSYDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTSMVGSTL 183
Db 121 ISHWLGATECVLLATMSYDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTSMVGSTL 180
QY 184 TMLPLCGNCCIDHFFCEMPLIMQLACVDTSLNMEMMYLASFVFFVPLPLGLILVSYGHIA 243
Db 181 TMLPLCGNCCIDHFFCEMPLIMQLACVDTSLNMEMMYLASFVFFVPLPLGLILVSYGHIA 240
QY 244 RAVLKIRSAEGRRKAFNTCSSHVAVVSLFYGSIIIFMYLQPAKSTSHQKGFIALFYTVVT 303
Db 241 RAVLKIRSAEGRRKAFNTCSSHVAVVSLFYGSIIIFMYLQPAKSTSHQKGFIALFYTVVT 300
QY 304 PALNPLIYTLRNTSVKALRMVLENCNCCSAGKLAQI 340
Db 301 PALNPLIYTLRNTSVKALRMVLENCNCCSAGKLAQI 337
RESULT 6
ABP95893
ID ABP95893 standard; protein; 377 AA.
XX ABP95893;
XX 06-MAR-2003 (first entry)
XX Human GPCR polypeptide SEQ ID NO 596.
DE Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
XX drug development; gustatory; taste; fragrance; receptor.
XX
```

```
OS Homo sapiens.
XX WO200216548-A2.
XX 28-FEB-2002.
XX 30-JUL-2001; 2001WO-IB001446.
XX 04-AUG-2000; 2000JP-00237818.
XX 13-FEB-2001; 2001JP-00034434.
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX Haga T, Takeda S, Mitaku S;
XX WPI; 2002-304118/34.
XX N-PSDB; ABZ43167.
XX Database global search for G protein-coupled receptors, proteins and
XX encoded genes for studying in vivo signal transduction mechanism and
XX identifying targets for drug development.
XX Claim 10; SEQ ID NO 596; 97pp + Sequence Listing; Japanese.
XX The invention relates to a method for screening G protein-coupled
XX receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95596-
XX ABP95942) by extracting open-reading frames containing 6-8 transmembrane
XX domains with 250-1000 amino acid residues to give a gene homologous with
XX a known GPCR gene. The receptor proteins and encoded genes are useful for
XX studying in vivo signal transduction mechanism and identifying targets
XX for drug development e.g. based on olfactory and gustatory receptors in
XX form of agonists and antagonists by screening intrinsic and extrinsic
XX ligands as bitter taste inhibitors, taste enhancers and fragrance
XX improvers. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 377 AA;
Query Match 97.1%; Score 1725; DB 5; Length 377;
Best Local Similarity 99.4%; Pred. No. 1.3e-181;
Matches 332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7 ALPTGGLLPHPQHTMMEIANVSSPEVFLVLLGFSARPSLETVLFIVVLSFYMVSILNGII 66
Db 44 ALPTGGLLPHPQHTMMEIANVSSPEVFLVLLGFSARPSLETVLFIVVLSFYMVSILNGII 103
QY 67 ILVSHTDVLHHTPMYFFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSISYGGCVVQFYISH 126
Db 104 ILVSHTDVLHHTPMYFFFLANLPFLDMSFTTSIVPQLLANLWGPQKTSISYGGCVVQFYISH 163
QY 127 WLGATECVLLATMSYDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTSMVGSTLTML 186
Db 164 WLGATECVLLATMSYDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTSMVGSTLTML 223
QY 187 LPLCGNCCIDHFFCEMPLIMQLACVDTSLNMEMMYLASFVFFVPLPLGLILVSYGHIA 246
Db 224 LPLCGNCCIDHFFCEMPLIMQLACVDTSLNMEMMYLASFVFFVPLPLGLILVSYGHIA 283
QY 247 LKIRSAEGRRKAFNTCSSHVAVVSLFYGSIIIFMYLQPAKSTSHQKGFIALFYTVVTPAL 306
Db 284 LKIRSAEGRRKAFNTCSSHVAVVSLFYGSIIIFMYLQPAKSTSHQKGFIALFYTVVTPAL 343
QY 307 NPLIYTLRNTSVKALRMVLENCNCCSAGKLAQI 340
Db 344 NPLIYTLRNTSVKALRMVLENCNCCSAGKLAQI 377
RESULT 7
ABR63708
ID ABR63708 standard; protein; 320 AA.
XX ABR63708;
XX
```

XX DT 29-SEP-2003 (first entry)
XX DE Human G-protein coupled receptor BCA-GPCR3-C.
XX KW Human; G-protein coupled receptor; BCA-GPCR-1; BCA-GPCR-2; BCA-GPCR-3;
KW BCA-GPCR-4; breast cancer; cytostatic; cancer; prostate cancer.
XX OS Homo sapiens.
XX PN WO2003054542-A1.
XX PD 03-JUL-2003.
XX PF 18-DEC-2002; 2002WO-US041112.
XX PR 20-DEC-2001; 2001US-00028521.
XX PA (TULA-) TULARIK INC.
XX PI Powers S, Yang J, Cutler G;
XX WPI; 2003-569288/53.
DR N-PSDB; ACC85516.
XX PT New G-protein coupled receptor (GPCR) polypeptides and nucleic acids,
PT useful for treating cancer, e.g. breast or prostate cancer.
XX PS Claim 10; Page 65; 77pp; English.
XX CC The present invention provides the protein and coding sequences of four
CC novel human G-protein coupled receptors (GPCR) which are amplified in
CC breast cancers. The sequences are useful in the treatment of cancers,
CC including breast and prostate cancers. The present sequence is a GPCR of
CC the invention
XX SQ Sequence 320 AA;
Query Match 93.1%; Score 1654; DB 6; Length 320;
Best Local Similarity 100.0%; Pred. No. 7.3e-174;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 21 MMEIANVSSPEVFLGFSARPSLETVLFIIVLSFYMVSILGNGIILVSHTDVHLHTPM 80
Db 1 MMEIANVSSPEVFLGFSARPSLETVLFIIVLSFYMVSILGNGIILVSHTDVHLHTPM 60
Qy 81 YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVVQFYISHWLGATECVLLATMS 140
Db 61 YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVVQFYISHWLGATECVLLATMS 120
Qy 141 YDRYAAICRPLHYTVIMHPQLCLGLALASWLGLTSMVGSTLTMLPLCGNCCIDHFFC 200
Db 121 YDRYAAICRPLHYTVIMHPQLCLGLALASWLGLTSMVGSTLTMLPLCGNCCIDHFFC 180
Qy 201 EMPLIMQLACVDTSLNEMEMYLASFVVFVVLPLGLILVSYGHIAARAVLKIRSAEGRRKAEN 260
Db 181 EMPLIMQLACVDTSLNEMEMYLASFVVFVVLPLGLILVSYGHIAARAVLKIRSAEGRRKAEN 240
Qy 261 TCSSHVAVVSLFYGSIIFMYLQPAKSTSHEQKFIALFYTVVTPALNPLIYTLRNTEVKS 320
Db 241 TCSSHVAVVSLFYGSIIFMYLQPAKSTSHEQKFIALFYTVVTPALNPLIYTLRNTEVKS 300
Qy 321 ALRHMVLECCGSAGKLAQI 340
Db 301 ALRHMVLECCGSAGKLAQI 320
RESULT 8
ID ABG66931
XX AC ABG66931 standard; protein; 320 AA.
XX AC ABG66931;
XX

DT 24-SEP-2002 (first entry)
XX Novel G-protein coupled receptor related protein #8.
DE
XX G protein coupled receptor; GPCR; olfactory receptor;
KW cell signal processing disorder; metabolic pathway modulation;
KW cardiomyopathy; atherosclerosis; diabetes; developmental disease;
KW immune disease; taste disorder; scent detectability disorder; obesity;
KW Burkitt's lymphoma; corticosterogenic disease; infectious disease; pain;
KW signal transduction pathway disorder; metabolic pathway disorder;
KW retinal disease; metabolic disorder; cancer; Parkinson's disease;
KW acute heart failure; urinary retention; osteoporosis; Crohn's disease;
KW ulcer; allergy; neurological disorder; genetic disorder; transplantation;
KW fertility; Pancreatitis; Hyperthyroidism; Endometriosis;
KW forensic biology; transgenic animal.
XX
OS Homo sapiens.
XX WO200240539-A2.
PN
XX 23-MAY-2002.
PD
XX 16-OCT-2001; 2001WO-US032256.
PF
XX 16-OCT-2000; 2000US-0240704P.
PR 26-OCT-2000; 2000US-0243497P.
PR 31-OCT-2000; 2000US-0244542P.
PR 03-NOV-2000; 2000US-0245484P.
PR 12-DEC-2000; 2000US-0255017P.
PR 17-JAN-2001; 2001US-0262159P.
PR 22-JAN-2001; 2001US-0263216P.
PR 22-JAN-2001; 2001US-0263340P.
PR 25-JAN-2001; 2001US-0264118P.
PR 12-FEB-2001; 2001US-0268225P.
PR 15-FEB-2001; 2001US-0269031P.
PR 27-JUL-2001; 2001US-0308203P.
XX
PA (CURA-) CURAGEN CORP.
XX Kekuda R, Spytek KA, Casman SJ, Zerhusen BD, Li L, Tchernev VT;
PI Colman SD, Ballinger RA, Padigaru M, Wolenc AR, Shenoy SG;
PI Edinger SR, Gerlach V, Gangolli EA, Macdougall JR, Smithson G;
PI Peyman JA, Stone DJ, Gunther E, Ellerman K, Grosse WM, Alsobrook JP;
PI Lepley DM, Burgess CE;
XX WPI; 2002-500205/53.
DR N-PSDB; ABK95449.
XX
PT Novel G protein coupled receptor especially olfactory receptor
PT polypeptides and nucleic acids for diagnosing and treating
PT atherosclerosis, cardiomyopathy and diabetes.
XX
PS Claim 1; Page 31; 309pp; English.
XX
CC The invention describes an isolated G protein coupled receptor X (GPCR1-
CC 12) polypeptide, especially an olfactory receptor. GPCR polypeptides are
CC useful for identifying an agent that binds to the polypeptide and for
CC identifying a candidate substance or ligand molecules interacting with an
CC olfactory receptor polypeptide. The polypeptide, (I) and (II) are also
CC useful for treating diseases and disorders related to cell signal
CC processing and metabolic pathway modulation e.g. cardiomyopathy,
CC atherosclerosis and diabetes, and developmental diseases, immune
CC diseases, taste and scent detectability disorders, Burkitt's lymphoma,
CC corticosterogenic disease, signal transduction pathway disorders,
CC metabolic pathway disorders, retinal diseases, metabolic disorders,
CC obesity, infectious disease, pain, cancer, Parkinson's disease, acute
CC heart failure, urinary retention, osteoporosis, Crohn's disease, ulcers,
CC allergies, neurological disorders, genetic disorders, transplantation,
CC fertility, Pancreatitis, Hyperthyroidism and Endometriosis. GPCR
CC sequences are also useful for identifying a cell or tissue type in a
CC biological sample, to amplify DNA sequences from very small biological
CC samples such as tissues e.g. hair or skin or body fluids in forensic
CC biology. Cells comprising (I) are useful for producing non-human

CC transgenic animals for studying the function and/or activity of GPCR
CC protein and for identifying and/or evaluating modulators of GPCR protein
CC activity. This is the amino acid sequence of a novel G-protein coupled
CC receptor described in the invention
XX
SQ Sequence 320 AA;

Query Match 93.0%; Score 1651; DB 5; Length 320;
Best Local Similarity 99.7%; Pred. No. 1.6e-173;
Matches 319; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 21 MMEIANVSSPEVFLGFSARPSLETFLFIVLSFYMVSIILGNGIILVSHDTHLTPM 80
Db 1 MMEIANVSSPEVFLGFSARPSLETFLFIVLSFYMVSIILGNGIILVSHDTHLTPM 60
QY 81 YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSISYGGCVVQFYISHWLGATECVLLATMS 140
Db 61 YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSISYGGCVVQFYISHWLGATECVLLATMS 120
QY 141 YDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVMGSLTLMLLPLCGNNCIDHFFC 200
Db 121 YDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVMGSLTLMLLPLCGNNCIDHFFC 180
QY 201 EMPLIMQLACVDTSLNEMEMYLASFVFWLPLGLILVSYGHIAARAVLKIRSAEGRKAFN 260
Db 181 EMPLIMQLACVDTSLNEMEMYLASFVFWLPLGLILVSYGHIAARAVLKIRSAEGRKAFN 240
QY 261 TCSSHVAVVSLFYGSIIFMYLQPAKSTSHEQGFIALFYVTPALNPLIYTLRNTVEKS 320
Db 241 TCSSHVAVVSLFYGSIIFMYLQPAKSTSHEQGFIALFYVTPALNPLIYTLRNTVEKS 300
QY 321 ALRHMVLENC CGSAGKLAQI 340
Db 301 ALRHMVLENC CGSAGKLAQI 320

RESULT 9
ABR63709
ID ABR63709 standard; protein; 319 AA.

XX ABR63709;
AC ABR63709;
DT 29-SEP-2003 (first entry)
XX Human G-protein coupled receptor BCA-GPCR3-D.
XX Human; G-protein coupled receptor; BCA-GPCR-1; BCA-GPCR-2; BCA-GPCR-3;
KW BCA-GPCR-4; breast cancer; cytostatic; cancer; prostate cancer.
XX Homo sapiens.
OS WO2003054542-A1.
PN 03-JUL-2003.
XX 18-DEC-2002; 2002WO-US041112.
PF 20-DEC-2001; 2001US-00028521.
XX (TULA-) TULARIK INC.
PA Powers S, Yang J, Cutler G;
XX WPI; 2003-569288/53.
PI N-PSDB; ACC85517.
DR New G-protein coupled receptor (GPCR) polypeptides and nucleic acids,
XX useful for treating cancer, e.g. breast or prostate cancer.
PT Claim 10; Page 66; 77pp; English.
PS The present invention provides the protein and coding sequences of four
XX novel human G-protein coupled receptors (GPCR) which are amplified in

CC breast cancers. The sequences are useful in the treatment of cancers,
CC including breast and prostate cancers. The present sequence is a GPCR of
CC the invention
XX
SQ Sequence 319 AA;

Query Match 92.8%; Score 1649; DB 6; Length 319;
Best Local Similarity 100.0%; Pred. No. 2.6e-173;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 MEIANVSSPEVFLGFSARPSLETFLFIVLSFYMVSIILGNGIILVSHDTHLTPMY 81
Db 1 MEIANVSSPEVFLGFSARPSLETFLFIVLSFYMVSIILGNGIILVSHDTHLTPMY 60
QY 82 FFLANLSFLDMSFTTSIVPQLLANLWGPQKTSISYGGCVVQFYISHWLGATECVLLATMSY 141
Db 61 FFLANLSFLDMSFTTSIVPQLLANLWGPQKTSISYGGCVVQFYISHWLGATECVLLATMSY 120
QY 142 DRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVMGSLTLMLLPLCGNNCIDHFFCE 201
Db 121 DRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVMGSLTLMLLPLCGNNCIDHFFCE 180
QY 202 MPLIMQLACVDTSLNEMEMYLASFVFWLPLGLILVSYGHIAARAVLKIRSAEGRKAFNT 261
Db 181 MPLIMQLACVDTSLNEMEMYLASFVFWLPLGLILVSYGHIAARAVLKIRSAEGRKAFNT 240
QY 262 CSSHVAVVSLFYGSIIFMYLQPAKSTSHEQGFIALFYVTPALNPLIYTLRNTVEKSA 321
Db 241 CSSHVAVVSLFYGSIIFMYLQPAKSTSHEQGFIALFYVTPALNPLIYTLRNTVEKSA 300
QY 322 LRHMVLENC CGSAGKLAQI 340
Db 301 LRHMVLENC CGSAGKLAQI 319

RESULT 10
ABJ04731
ID ABJ04731 standard; protein; 320 AA.

XX ABJ04731;
AC ABJ04731;
DT 16-OCT-2002 (first entry)
XX GPCR 11 protein SEQ ID No 28.
DE Antidiabetic; cytostatic; anorectic; nootropic; neuroprotective; GPCR;
KW antiparkinsonian; cardiac; antiarteriosclerotic; immunosuppressive;
KW hypotensive; haemostatic; antifertility; antiasthmatic; antiinflammatory;
KW anti-HIV; G-protein coupled receptor X; cardiomyopathy; atherosclerosis;
KW diabetes; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; neurodegenerative disorder; Alzheimer's disease; dyslipidaemia;
KW parkinson's disorder; immune disorder; haematopoietic disorder; obesity;
KW metabolic syndrome X; wasting disorder; cancer; hypertension; neoplasm;
KW congenital heart defect; aortic stenosis; subaortic stenosis; lymphoma;
KW transplantation; adrenoleukodystrophy; congenital adrenal hyperplasia;
KW prostate cancer; adenocarcinoma; uterus cancer; fertility; haemophilia;
KW hypercoagulation; idiopathic thrombocytopenic purpura; immunodeficiency;
KW graft versus host disease; AIDS; bronchial asthma; Crohn's disease;
KW multiple sclerosis; chromosomal mapping; tissue typing; forensic biology;
KW gene therapy; transgenic animal.
XX Unidentified.
OS WO200246229-A2.
XX 13-JUN-2002.
PN 05-DEC-2001; 2001WO-US046530.
XX 05-DEC-2000; 2000US-0251459P.
PR 29-DEC-2000; 2000US-0259007P.
XX 04-DEC-2001; 2001US-00005041.
XX

Db	301	ALRHMVLECCGSAGKLAQI	320	
RESULT 12				
AAG71912				
ID	AAG71912	standard; protein; 319 AA.		
XX	AC	AAG71912;		
XX	AC	AAG71912;		
DT	30-JUL-2001	(first entry)		
XX				
DE		Human olfactory receptor polypeptide, SEQ ID NO: 1593.		
XX				
KW		Human; olfactory receptor; OR; primary scent determination;		
KW		secondary scent determination; polypeptide library; odour receptor;		
KW		scent profile; scent fingerprint; scent representation.		
XX				
OS		Homo sapiens.		
XX				
PN	WO200127158-A2;			
XX				
PD	19-APR-2001.			
XX				
PF	06-OCT-2000; 2000WO-US027582.			
XX				
PR	08-OCT-1999; 99US-0158615P.			
PR	24-FEB-2000; 2000US-0184809P.			
XX				
PA	(DIGI-) DIGISCENTS.			
PA	(YEDA) YEDA RES & DEV CO LTD.			
XX				
PI	Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;			
DR	WPI; 2001-290713/30.			
XX				
PT	New polynucleotides which encode polypeptides involved in olfactory			
PT	sensation for identifying olfactory agonists and antagonists.			
XX				
PS	Claim 11; Page 1029-1030; 1857pp; English.			
XX				
CC	The present sequence is an olfactory receptor which is encoded by one of			
CC	a number of novel polynucleotides. The polynucleotides can be used in			
CC	screening for olfactory agonists and antagonists. The methods allow for			
CC	the determination of primary scents and the identification of the odour			
CC	receptors used to detect these primary scents. The methods also enable			
CC	determination of secondary scents and the identification of combinations			
CC	of odour receptors that are involved in detecting such secondary scents.			
CC	This enables the construction of a scent representation (also called a			
CC	scent fingerprint or scent profile), which may be used to re-create and			
CC	edit scents. Libraries of olfactory receptors are useful for determining			
CC	the interaction pattern of a composition with the receptors, and can be			
CC	used for determining differences in the olfactory faculties of different			
XX	individuals			
SQ	Sequence 319 AA;			
Query Match				
Best Local Similarity 92.4%; Score 1641; DB 4; Length 319;				
Matches 317; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
QY	21	MMEIANVSSPEVFVLLGFSARPSETLVLFIVVLSFYMVSIILVSHVLTVDVHLHTPM	80	
Db	1	MMEIANVSSPEVFVLLGFSARPSETLVLFIVVLSFYMVSIILVSHVLTVDVHLHTPM	60	
QY	81	YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVVQFVISHWLGATECVLLATMS	140	
Db	61	YFFLANLPFLDMSFTTSIVPQLLANLWGPQKTSYGGCVVQFVISHWLGATECVLLATMS	120	
QY	141	YDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVMGSTLTMLLPLCGNCCIDHFFC	200	
Db	121	YDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVMGSTLTMLLPLCGNCCIDHFFC	180	
QY	201	EMPLIMQLACVDTSLNEMEMYLASFVFFVPLPLGLILVSYGHIAVAVLKIRSAEGRKAFN	260	

Db	181	EMPLIMQLACVDTSLNEMEMYLASFVFFVPLPLGLILVSYGHIAVAVLKIRSAEGRKAFN	240	
QY	261	TCSSHVAVVSLFYGSIIFMYLQPAKSTSHQKGKFIALFYTVVTPALNPLIYTLRNTVEKS	320	
Db	241	TCSSHVAVVSLFYGSIIFMYLQPAKSTSHQKGKFIALFYTVVTPALNPLIYTLRNTVEKS	300	
QY	321	ALRHMVLECCGSAGKLAQ	339	
Db	301	ALRHMVLECCGSAGKLAQ	319	
RESULT 13				
AAG71896				
ID	AAG71896	standard; protein; 319 AA.		
XX	AC	AAG71896;		
XX	AC	AAG71896;		
DT	30-JUL-2001	(first entry)		
XX				
DE		Human olfactory receptor polypeptide, SEQ ID NO: 1577.		
XX				
KW		Human; olfactory receptor; OR; primary scent determination;		
KW		secondary scent determination; polypeptide library; odour receptor;		
KW		scent profile; scent fingerprint; scent representation.		
XX				
OS		Homo sapiens.		
XX				
PN	WO200127158-A2.			
XX				
PD	19-APR-2001.			
XX				
PF	06-OCT-2000; 2000WO-US027582.			
XX				
PR	08-OCT-1999; 99US-0158615P.			
PR	24-FEB-2000; 2000US-0184809P.			
XX				
PA	(DIGI-) DIGISCENTS.			
PA	(YEDA) YEDA RES & DEV CO LTD.			
XX				
PI	Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;			
XX				
DR	WPI; 2001-290713/30.			
XX				
PT	New polynucleotides which encode polypeptides involved in olfactory			
PT	sensation for identifying olfactory agonists and antagonists.			
XX				
PS	Claim 11; Page 1016; 1857pp; English.			
XX				
CC	The present sequence is an olfactory receptor which is encoded by one of			
CC	a number of novel polynucleotides. The polynucleotides can be used in			
CC	screening for olfactory agonists and antagonists. The methods allow for			
CC	the determination of primary scents and the identification of the odour			
CC	receptors used to detect these primary scents. The methods also enable			
CC	determination of secondary scents and the identification of combinations			
CC	of odour receptors that are involved in detecting such secondary scents.			
CC	This enables the construction of a scent representation (also called a			
CC	scent fingerprint or scent profile), which may be used to re-create and			
CC	edit scents. Libraries of olfactory receptors are useful for determining			
CC	the interaction pattern of a composition with the receptors, and can be			
CC	used for determining differences in the olfactory faculties of different			
XX	individuals			
SQ	Sequence 319 AA;			
Query Match				
Best Local Similarity 92.4%; Score 1641; DB 4; Length 319;				
Matches 317; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
QY	21	MMEIANVSSPEVFVLLGFSARPSETLVLFIVVLSFYMVSIILVSHVLTVDVHLHTPM	80	
Db	1	MMEIANVSSPEVFVLLGFSARPSETLVLFIVVLSFYMVSIILVSHVLTVDVHLHTPM	60	
QY	81	YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVVQFVISHWLGATECVLLATMS	140	
Db	61	YFFLANLPFLDMSFTTSIVPQLLANLWGPQKTSYGGCVVQFVISHWLGATECVLLATMS	120	
QY	141	YDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVMGSTLTMLLPLCGNCCIDHFFC	200	
Db	121	YDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVMGSTLTMLLPLCGNCCIDHFFC	180	
QY	201	EMPLIMQLACVDTSLNEMEMYLASFVFFVPLPLGLILVSYGHIAVAVLKIRSAEGRKAFN	260	

PN WO200259313-A2.
XX 01-AUG-2002.
PD 18-DEC-2001; 2001WO-US049394.
XX 18-DEC-2000; 2000US-0256635P.
PR 21-DEC-2000; 2000US-0257876P.
PR 04-JAN-2001; 2001US-0259743P.
PR 10-JAN-2001; 2001US-0260718P.
PR 12-JAN-2001; 2001US-0261498P.
PR 24-JAN-2001; 2001US-0263689P.
PR 08-FEB-2001; 2001US-0267464P.
PR 22-FEB-2001; 2001US-0271021P.
PR 14-MAR-2001; 2001US-0275946P.
PR 23-MAR-2001; 2001US-0278150P.
PR 18-APR-2001; 2001US-0284591P.
PR 23-APR-2001; 2001US-0285718P.
PR 19-JUN-2001; 2001US-0299327P.
PR 16-AUG-2001; 2001US-0312902P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Li L, Ballinger RA, Padigaru M, Kekuda R, Colman SD, Spytek KA;
PI Casman SJ, Vernet CAM, Shenoy SG, Gusev V, Malyankar UM, Edinger S;
PI Gerlach V, Smithson G, Stone DJ, Sciore P, Macdougall JR, Gunther E;
PI Peyman JA, Ellerman K, Gangolli EA, Millet I;
XX
DR WPI; 2002-599789/64.
DR N-PSDB; ABS58830.
XX
PT New G protein coupled receptor polypeptides and polynucleotides, useful
in gene therapy, particularly for treating or preventing cardiomyopathy,
atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer
in humans.
XX
PS Claim 9; Page 166; 685pp; English.
XX
CC The invention relates to novel isolated G-protein coupled receptor (GPCR)
polypeptides and polynucleotides. The GPCR polypeptide, GPCR nucleic acid
and antibody are useful for treating, preventing or alleviating a GPCR-
associated disorder or a pathological state in a subject, particularly a
human. In particular, the disorder is cardiomyopathy, atherosclerosis,
diabetes, or a disorder related to cell signal processing and metabolic
pathway modulation. The GPCR polypeptide and nucleic acid are also useful
for diagnosing the presence of or predisposition to a disease associated
with altered levels of GPCR, particularly cancer. The GPCR nucleic acid
and polypeptide are especially useful in therapeutic or prophylactic
applications for disorders associated with aberrant GPCR expression or
activity. The DNA encoding the protein is useful in gene therapy for
treating the above conditions. Furthermore, the nucleic acids and
polypeptides are useful in treating adenocarcinoma, lymphoma, prostate
cancer, uterus cancer, immune response, neurodegenerative disorders,
asthma, inflammatory disorders, Crohn's disease, multiple sclerosis or
Albright hereditary osteodystrophy. These are also useful in developing a
powerful assay system for functional analysis of various human disorders,
as well as in diagnostic applications. ABG76767-ABG76870 represent human
GPCR amino acid sequences of the invention
XX
SQ Sequence 314 AA;

Query Match 91.0%; Score 1617; DB 5; Length 314;
Best Local Similarity 99.4%; Pred. No. 8.8e-170;
Matches 312; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 21 MMEIANVSSPEVFLVLLGFSARPSLETIVLVLSFYMVSILNGIILVSHTDVHLTPM 80
Db 1 MMEIANVSSPEVFLVLLGFSARPSLETIVLVLSFYMVSILNGIILVSHTDVHLTPM 60
QY 81 YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVQVFIYSHWLGATECVLLATMS 140
Db 61 YFFLANLPFLDMSFTTSIVPQLLANLWGPQKTSYGGCVQVFIYSHWLGATECVLLATMS 120

QY 141 YDRYAAICRPLHYTVIMHPOLCLGLALASWLGGTLTSMVGSTLTMLLPLCGNNCIDHFFC 200
Db 121 YDRYAAICRPLHYTVIMHPOLCLGLALASWLGGTLTSMVGSTLTMLLPLCGNNCIDHFFC 180
QY 201 EMPLIMQLACVDTSLNEMEMYLASFVVFVPLGLLILVSYGHIAVAVLKIRSAEGRRKAFN 260
Db 181 EMPLIMQLACVDTSLNEMEMYLASFVVFVPLGLLILVSYGHIAVAVLKIRSAEGRRKAFN 240
QY 261 TCSSHVAVVSLFYGSIIFMYLQPAKSTSHQKGFIALFYTVVTPALNPLIYTLRNTVEKS 320
Db 241 TCSSHVAVVSLFYGSIIFMYLQPAKSTSHQKGFIALFYTVVTPALNPLIYTLRNTVEKS 300
QY 321 ALRHMVLENC CGSA 334
Db 301 ALRHMVLENC CGSA 314

Search completed: April 8, 2005, 17:08:27
Job time : 176 secs

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OM protein - protein search, using sw model

Run on: April 8, 2005, 16:54:13 ; Search time 46 Seconds
(without alignments)
711.167 Million cell updates/sec

Title: US-10-633-894-6
Perfect score: 1776
Sequence: 1 MPCMPCALPTGGLLPHPQHT.....ALRHMVLECCGSAGKLAQI 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	985	55.5	312	2 A46247	olfactory receptor
2	868	48.9	316	2 A57069	olfactory receptor
3	769	43.3	305	2 S29711	olfactory factor O
4	754	42.5	315	2 JC5836	olfactory receptor
5	713.5	40.2	318	2 JC5202	chemoreceptor TB64
6	682.5	38.4	313	2 S20571	olfactory receptor
7	681	38.3	314	2 S29707	olfactory receptor
8	676	38.1	313	2 B23701	olfactory receptor
9	674	38.0	319	2 JC5624	olfactory receptor
10	672	37.8	314	2 S20572	olfactory receptor
11	667	37.6	314	2 A37286	olfactory receptor
12	665	37.4	307	2 S29710	olfactory receptor
13	664	37.4	310	2 E23701	olfactory receptor
14	662	37.3	309	1 S51356	olfactory receptor
15	660	37.2	311	2 C23701	olfactory receptor
16	657	37.0	314	2 H23701	olfactory receptor
17	655	36.9	304	2 S29709	olfactory receptor
18	652	36.7	327	2 F23701	olfactory receptor
19	646	36.4	311	2 JC5200	chemoreceptor TB33
20	646	36.4	315	2 JC4658	olfactory receptor
21	644.5	36.3	312	2 A48413	probable olfactory
22	642	36.1	312	2 S29708	olfactory receptor
23	638	35.9	320	2 S20573	olfactory receptor
24	636	35.8	312	2 G23701	olfactory receptor
25	634	35.7	333	2 A23701	olfactory receptor
26	632	35.6	315	2 JC5201	chemoreceptor TB56
27	630	35.5	317	2 D23701	olfactory receptor
28	610	34.3	312	2 I23701	olfactory receptor
29	565	31.8	312	2 A46750	olfactory receptor

30	532	30.0	222	2 D40745	odorant receptor (
31	510	28.7	264	2 PC4369	olfactory receptor
32	497	28.0	222	2 B40745	odorant receptor (
33	493	27.8	157	2 S58035	probable olfactory
34	478	26.9	234	2 S29000	G protein-coupled
35	474	26.7	232	2 S29001	G protein-coupled
36	466	26.2	216	2 I38474	olfactory receptor
37	465.5	26.2	225	2 I38478	olfactory receptor
38	462	26.0	216	2 I38470	olfactory receptor
39	462	26.0	216	2 I38480	olfactory receptor
40	461.5	26.0	154	2 S58070	probable olfactory
41	455	25.6	216	2 I38476	olfactory receptor
42	452	25.5	234	2 S28998	G protein-coupled
43	450.5	25.4	328	2 G45774	odorant receptor 2
44	448	25.2	216	2 I38479	olfactory receptor
45	432	24.3	216	2 I38477	olfactory receptor

ALIGNMENTS

RESULT 1

A46247

olfactory receptor OR3 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A46247

R;Nef, P.; Hermans-Borgmeyer, I.; Artieres-Pin, H.; Beasley, L.; Dionne, V.E.; Heinemann

Proc. Natl. Acad. Sci. U.S.A. 89, 8948-8952, 1992

A;Title: Spatial pattern of receptor expression in the olfactory epithelium.

A;Reference number: A46247; MUID:93028384; PMID:1384038

A;Accession: A46247

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-312 <NEP>

A;Cross-references: UNIPROT:P23275; GB:M84005; NID:g200153; PIDN:AAA39862.1; PID:g200154

A;Note: sequence extracted from NCBI backbone (NCBIP:115362)

C;Superfamily: olfactory receptor OR14

Query Match 55.5%; Score 985; DB 2; Length 312;
Best Local Similarity 60.0%; Pred.No. 8.1e-77;
Matches 183; Conservative 50; Mismatches 72; Indels 0; Gaps 0;

Qy	22	MEIANVSSPEVFLVLLGFSARPSLETVLFIVVLSFYMVSIILNGIILVSHTDVHLHTPMY	81
Db	1	MEVDSNSSSGTFILMGVSDHPHLEIFFAVILASYLLTLVGNLTIIILSRDLARLHTPMY	60
Qy	82	FFLANLSFLDMSFTTSIVPQLLANLWGPQKTISYGGCVVQFYISHWLGATECVLLATMSY	141
Db	61	FFLSNLSSLDLAFTTSSVPQMLKNLWGPDKTISYGGCVTQLYVFLWLGATECILLVVMF	120
Qy	142	DRYAAICRPLHYTVIMHPQLCLGLALASWLGLTTSMVGSTLMLPLCGNNCIDHFFCE	201
Db	121	DRYVAVCRPLHYMTVMNPRLCWGLAAISWLGGLGNSVIQSTFTTLQLPFCGHRKVDNFLCE	180
Qy	202	MPLIMQLACVDTSLNEMEMYLASFVFWVPLPLGLILVSYGHIARAVLKIRSAEGRRKAFNT	261
Db	181	VPAMIKLACGDTSLNEAVLNGVCTFTTVVPVSVILVSYCFIAQAVMKIRSVEGRRKAFNT	240
Qy	262	CSSHVAVVSLFYGSIIFMYLQPAKSTSHQGFIALFYTVVTPALNPLIYTLRNTEVKSA	321
Db	241	CVSHLVVFLFYGSAIYGILLPAKSSNQSGKFISLFYSVVTMVPNPLIYTLRNKEVKA	300
Qy	322	LRHNV	326
Db	301	LGRL	305

RESULT 2

A57069

olfactory receptor PAT11 - human

C;Species: Homo sapiens (man)

C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004

A;Status: preliminary; nucleic acid sequence not shown	
A;Molecule type: DNA	
A;Residues: 1-318 <THO1>	
A;Cross-references: UNIPROT:Q62944; GB:U50949; NID:g1256392; PIDN:AAC52911.1; PID:g12563	
A;Accession: PC4304	
A;Status: preliminary	
A;Molecule type: protein	
A;Residues: 145-153;245-253 <THO2>	
A;Experimental source: taste bud	
C;Comment: This protein is coupled to a GTP-binding protein-mediated signal transduction	
C;Genetics:	
A;Gene: tb641	
C;Superfamily: olfactory receptor OR14	
C;Keywords: olfaction; taste bud; transmembrane protein	
F;30-53/Domain: transmembrane #status predicted <TM1>	
F;63-84/Domain: transmembrane #status predicted <TM2>	
F;106-125/Domain: transmembrane #status predicted <TM3>	
F;145-169/Domain: transmembrane #status predicted <TM4>	
F;202-224/Domain: transmembrane #status predicted <TM5>	
F;243-265/Domain: transmembrane #status predicted <TM6>	
F;276-296/Domain: transmembrane #status predicted <TM7>	
Query Match 40.2%; Score 713.5; DB 2; Length 318;	
Best Local Similarity 46.9%; Pred. No. 1.4e-53;	
Matches 138; Conservative 59; Mismatches 94; Indels 3; Gaps 2;	
QY	33 FVLLGFSARPSLETVLFIVVLSFYVMVSIILNGIILVSHWLGATECVLLATMSYDRYAACRPL 91
Db	16 FLLGLAHPNLRTFLELVFLLIYILTQNLILLTVWADPKLHARPMYILLGVLSFLD 75
QY	92 MSFTTSIVPQLLANLWGPQKTISYGGCVVQFYISHWLGATECVLLATMSYDRYAACRPL 151
Db	76 MWLSSVIVPRIILNFTPANKAIAFGGCVAQLYFFHFLGSTQCFLYTLMAYDRYLAICQPL 135
QY	152 HYTVIMHPQLCLGLALASWLGGLTTSVMGSTLTMLPLCGNNCIDHFFCEMPLIMQLACV 211
Db	136 RYPVLMNGKLCTIILVAGAWVAGSIQATLTFRLPYCGPKEVDYFFCDIPAVLRLACA 195
QY	212 DTSLNEMEMYLASFVFVVLPLGLILVSYGHIARAVLKIRSAEGRRKAFNTCSSHVAVVSL 271
Db	196 DTAINELTVFDIGVVAASCFLLILLSYANIVHAILKIRTADGRRRAFEFCGSHLTVTV 255
QY	272 FYGSIIFMYLQPAKSTSHEQGKFIALFYTVVTPALNPLIYTLRNTVEKSAIRHM 325
Db	256 YVVCIFIYLRAGSKSSFDA--VAVFYTVVTPLNPLIYTLRNQEVNSALKRL 307
RESULT 6	
S20571	
olfactory receptor - dog	
C;Species: Canis lupus familiaris (dog)	
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004	
C;Accession: S20571	
R;Parmentier, M.; Libert, F.; Schurmans, S.; Schiffmann, S.; Lefort, A.; Eggerickx, D.;	
Nature 355, 453-455, 1992	
A;Title: Expression of members of the putative olfactory receptor gene family in mammali	
A;Reference number: S20571; MUID:92131132; PMID:1370859	
A;Accession: S20571	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-313 <PAR>	
A;Cross-references: UNIPROT:P30955; EMBL:X64996; NID:g890; PIDN:CAA46129.1; PID:g891	
C;Superfamily: olfactory receptor OR14	
C;Keywords: G protein-coupled receptor; transmembrane protein	
Query Match 38.4%; Score 682.5; DB 2; Length 313;	
Best Local Similarity 44.6%; Pred. No. 6.2e-51;	
Matches 131; Conservative 60; Mismatches 102; Indels 1; Gaps 1;	
QY	33 FVLLGFSARPSLETVLFIVVLSFYVMVSIILNGIILVSHWLTDVHLHTPMYFFLANLSFLDM 92
Db	12 FVLLGLPIDPDQBDLFYALFLAMYVTTILGNLLIIVLIQLDLSHLHTPMYFLSNLSFSDL 71

QY	93 SFTTSIVPQLLANLWGPQKTISYGGCVVQFYISHWLGATECVLLATMSYDRYAACRPLH 152
Db	72 CFSSVTMPKLLQNMQSQVPSIPYAGCLTQMYFFLFFGDLESFLLVAMAYDRYVAICFPLH 131
QY	153 YTVMHPQLCLGLALASWLGGLTTSVMGSTLTMLPLCGNNCIDHFFCEMPLIMQLACVD 212
Db	132 YTTIMSPKLCFSLVLVSWVLTMFHAVLHTLLMARLFCFANT-IPHFFCDMSALLKLACSD 190
QY	213 TSLNEMEMYLASFVFVVLPLGLILVSYGHIARAVLKIRSAEGRRKAFNTCSSHVAVVSLF 272
Db	191 TQVNELVIFIMGGLILVIPFLLIITSYARIIVSSILKVPISAIGICKVFSTCGSHLSVVSLF 250
QY	273 YGSIIFMYLQPAKSTSHEQGKFIALFYTVVTPALNPLIYTLRNTVEKSAIRHMV 326
Db	251 YGTVIGLYLCPSSANNSTVKETIMAMMYTVVTPMLNPFYISLRNKDMKGALRRVI 304
RESULT 7	
S29707	
olfactory receptor OR5 - rat	
C;Species: Rattus norvegicus (Norway rat)	
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004	
C;Accession: S29707; B37286	
R;Raming, K.; Krieger, J.; Strotmann, J.; Boekhoff, I.; Kubick, S.; Baumstark, C.; Breer	
Nature 361, 353-356, 1993	
A;Title: Cloning and expression of odorant receptors.	
A;Reference number: S29707; MUID:93149273; PMID:7678922	
A;Accession: S29707	
A;Molecule type: mRNA	
A;Residues: 1-314 <RAM>	
A;Cross-references: UNIPROT:Q04059	
R;Buck, L.; Axel, R.	
Cell 65, 175-187, 1991	
A;Title: A novel multigene family may encode odorant receptors: a molecular basis for od	
A;Reference number: A23701; MUID:91191556; PMID:1840504	
A;Accession: B37286	
A;Status: nucleic acid sequence not shown; not compared with conceptual translation	
A;Molecule type: mRNA	
A;Residues: 193-236 <BUC>	
A;Cross-references: GB:M64375; NID:g205811; PIDN:AAA41738.1; PID:g205812	
C;Superfamily: olfactory receptor OR14	
C;Keywords: G protein-coupled receptor; membrane protein	
Query Match 38.3%; Score 681; DB 2; Length 314;	
Best Local Similarity 45.5%; Pred. No. 8.4e-51;	
Matches 133; Conservative 62; Mismatches 93; Indels 4; Gaps 2;	
QY	33 FVLLGFSARPSLETVLFIVVLSFYVMVSIILNGIILVSHWLTDVHLHTPMYFFLANLSFLDM 92
Db	12 FLLGLPIPEHQHFYALFLSMYLTTLGNLIILILLDSHLHTPMYFLSNLSFSDL 71
QY	93 SFTTSIVPQLLANLWGPQKTISYGGCVVQFYISHWLGATECVLLATMSYDRYAACRPLH 152
Db	72 CFSSVTMPKLLQNMQSQVPSIPYAGCLSIQYFFLFFGDLGNFLLVAMAYDRYVAICFPLH 131
QY	153 YTVMHPQLCLGLALASWLGGLTT--SMVGSTLTMLPLCGNNCIDHFFCEMPLIMQLAC 210
Db	132 YMSIMSPKLCVSLVVLVSWV--LTTTFHAMLHTLLMARLSFCEDNVIPHFCDMSALLKLAC 189
QY	211 VDTSLNEMEMYLASFVFVVLPLGLILVSYGHIARAVLKIRSAEGRRKAFNTCSSHVAVVS 270
Db	190 SDTRVNEVVFIFVWSLFLVLPFALIIMSXYRIVSSILKVPSSQGIYKAFSSCGSHLSVVS 249
QY	271 LFYGSIIFMYLQPAKSTSHEQGKFIALFYTVVTPALNPLIYTLRNTVEKSAI 322
Db	250 LFYGTVIPLYLCPSSNNSTVKETVMSLMYTLVTPMLNPFYISLRNRDIKGAM 301
RESULT 8	
B23701	
olfactory receptor F5 - rat	
C;Species: Rattus norvegicus (Norway rat)	
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 04-Sep-1998	

C;Accession: B23701
R;Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A;Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A;Reference number: A23701, MUID:91191556; PMID:1840504
A;Accession: B23701
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-313 <BUC>
A;Cross-references: GB:M64377
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 38.1%; Score 676; DB 2; Length 313;
Best Local Similarity 45.3%; Pred. No. 2.2e-50;
Matches 139; Conservative 57; Mismatches 107; Indels 4; Gaps 2;

QY 22 MEIANVSSPEVFLGFSARPSLETVLFIVVLSFYMVSIILGNGIILVSHTDVHLHTPMY 81
Db 1 MSSTNQSSVTEFLGLSLRQPQQQLLFLFLIMYLATVLGNLLIILAIGTDSRLHTPMY 60

QY 82 FFLANLSFLDMSFTTSIVPQLLANLWGPQKTIISYGGCVVQFYISHWLGATECVLLATMSY 141
Db 61 FFLSNLSFVDVCFSSSTTVPKVLANHILGSAISFGCLTQLYFLAVFGNMDNFFLLAVMSY 120

QY 142 DRYAAICRPLHYTVIMHPQCLGLALASWLGGLTTSVMGSLTMLLPLCGNCCIDHFFCE 201
Db 121 DRFVAICHELPHYTTKMTROQLCVLLVVGSWVANMNCILLHILLMARKSFCDNMIPHFCD 180

QY 202 MPLIMQACVDTSLNEMEMYLASFVFWVPLPLGLILVSYGHIARAVLKIRSAEGRKAFNT 261
Db 181 GTPLKLKSCSDTHLNELMILTEGAVVMVTPFVCILISYIHITCAVLRVSSPRGWSFST 240

QY 262 CSSHVAVVSFLFYGSIIFMYLOPAKSTSHQKFI--ALFYTVVTPALNPLIYTLRNTQVK 319
Db 241 CGSHLAVVCLFYGTAVIYFNP--SSSHLAGRDMAAAVVAVVTPMLNPFYSLRNSDMK 298

QY 320 SALRHMV 326
Db 299 AALRKVL 305

RESULT 9
JC5624
olfactory receptor HTPCR92 - human
C;Species: Homo sapiens (man)
C;Date: 14-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Accession: JC5624; S58003
R;Vanderhaeghen, P.; Schurmans, S.; Vassart, G.; Parmentier, M.
Biochem. Biophys. Res. Commun. 237, 283-287, 1997
A;Title: Molecular cloning and chromosomal mapping of olfactory receptor genes expressed
A;Reference number: JC5624; MUID:97415789; PMID:9268701
A;Contents: Testis
A;Accession: JC5624
A;Molecule type: mRNA
A;Residues: 1-319 <VAN>
A;Cross-references: UNIPROT:Q15622; GB:Y10530; NID:G2792017; PIDN:CAA71558.1; PID:G27920
R;Vanderhaeghen, P.; Schurmans, S.; Vassart, G.; Parmentier, M.
submitted to the EMBL Data Library, July 1995
A;Description: Male germ cells from several mammalian species express a specific reperto
A;Reference number: S57995
A;Accession: S58003
A;Molecule type: mRNA
A;Residues: 126-282 <VAV>
A;Cross-references: EMBL:X89677; NID:G902337; PIDN:CAA61824.1; PID:G902338
C;Genetics:
A;Map position: 19p13.1
C;Function:
A;Description: involved in control of sperm physiology
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein
F;26-48/Domain: transmembrane #status predicted <TM1>
F;58-79/Domain: transmembrane #status predicted <TM2>

F;101-120/Domain: transmembrane #status predicted <TM3>
F;140-164/Domain: transmembrane #status predicted <TM4>
F;197-218/Domain: transmembrane #status predicted <TM5>
F;237-260/Domain: transmembrane #status predicted <TM6>
F;272-292/Domain: transmembrane #status predicted <TM7>

Query Match 38.0%; Score 674; DB 2; Length 319;
Best Local Similarity 45.8%; Pred. No. 3.4e-50;
Matches 138; Conservative 53; Mismatches 110; Indels 0; Gaps 0;

QY 22 MEIANVSSPEVFLGFSARPSLETVLFIVVLSFYMVSIILGNGIILVSHTDVHLHTPMY 81
Db 1 MEPGNDTQISEFLLLGFSQEPGLQPFGLFSLMYLVTVLGNLLIILATISDSHLHTPMY 60

QY 82 FFLANLSFLDMSFTTSIVPQLLANLWGPQKTIISYGGCVVQFYISHWLGATECVLLATMSY 141
Db 61 FFLSNLSFADICVTSTTIPKMLMNIQONKVITYIACLMQMYFFILFAGFENFLLSV MAY 120

QY 142 DRYAAICRPLHYTVIMHPQCLGLALASWLGGLTTSVMGSLTMLLPLCGNCCIDHFFCE 201
Db 121 DRFVAICHELPHYVMIMPHLCGLVLASWTMSALYSLLQILMVVRLSFCTALEIPHFCE 180

QY 202 MPLIMQACVDTSLNEMEMYLASFVFWVPLPLGLILVSYGHIARAVLKIRSAEGRKAFNT 261
Db 181 LNQVIQLACSDSFLNHMVIYFTVALLGGGLTGILYSYKISSIHAISSAQGYKAFST 240

QY 262 CSSHVAVVSFLFYGSIIFMYLOPAKSTSHQKFI--ALFYTVVTPALNPLIYTLRNTQVKSA 321
Db 241 CASHLSVVSFLFYGAILGVYLLSSAATRNSSHSSATASVMYTVVTPMLNPFYSLRNKDIKRA 300

QY 322 L 322
Db 301 L 301

RESULT 10
S20572
olfactory receptor - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S20572
R;Parmentier, M.; Libert, F.; Schurmans, S.; Schiffmann, S.; Lefort, A.; Eggerickx, D.; I
Nature 355, 453-455, 1992
A;Title: Expression of members of the putative olfactory receptor gene family in mamma
A;Reference number: S20571; MUID:92131132; PMID:1370859
A;Accession: S20572
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-314 <PAR>
A;Cross-references: UNIPROT:P30953; EMBL:X64994; NID:G32085; PIDN:CAA46127.1; PID:G32086
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 37.8%; Score 672; DB 2; Length 314;
Best Local Similarity 43.9%; Pred. No. 4.9e-50;
Matches 133; Conservative 62; Mismatches 104; Indels 4; Gaps 2;

QY 26 NVSSPEVFLGFSARPSLETVLFIVVLSFYMVSIILGNGIILVSHTDVHLHTPMYFFLA 85
Db 5 NQTSISDFLLGLGLPIQEQNLCYALFLAMYLTLLGNLLIIVILRLDLSHLHTPMYFLS 64

QY 86 NLSFLDMSFTTSIVPQLLANLWGPQKTIISYGGCVVQFYISHWLGATECVLLATMSYDRYA 145
Db 65 NLSFSDLCFSSVTIPKLLQNMQNQDPSIPYADCLTQMYFFLLFGDLSEFLLVAMAYDRYV 124

QY 146 AICRPLHYTVIMHPQCLGLALASWLGGLT--SMVGSLTMLLPLCGNCCIDHFFCEMP 203
Db 125 AICFPLHYTAIMSPMLCALVALSWV--LTTFFHAMLHTLLMARLFCADNVIPHFCDMS 182

QY 204 LIMQLACVDTSLNEMEMYLASFVFWVPLPLGLILVSYGHIARAVLKIRSAEGRKAFNTCS 263
Db 183 ALLKLAFSDBTRVNEWVIFIMGGGLIIVIPFLLILGYSARIIVSSILKVPSSKGICKAFSTCG 242

QY	264	SHVAVVSLFYGSIIFMYLQPAKSTSHQGGKFIALFYTVVTPALNPLIYTLRNTEVKSALR	323
Db	243	SHLSVVSIFYGTGILYLCSSANSSTLKDTVMAMMYTVVTPMLNPFYSLNRDMKGALS	302
QY	324	HMV	326
Db	303	RVI	305
RESULT 11			
A37286			
olfactory receptor I15 - rat			
C:Species: Rattus norvegicus (Norway rat)			
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004			
C:Accession: A37286			
R:Buck, L.; Axel, R.			
Cell 65, 175-187, 1991			
A:Title: A novel multigene family may encode odorant receptors: a molecular basis for od			
A:Reference number: A23701; MUID:91191556; PMID:1840504			
A:Accession: A37286			
A:Status: nucleic acid sequence not shown; not compared with conceptual translation			
A:Molecule type: mRNA			
A:Residues: 1-314 <BUC>			
A:Cross-references: UNIPROT:P23274; GB:M64392; NID:g205845; PIDN:AAA41755.1; PID:g205846			
C:Superfamily: olfactory receptor OR14			
C:Keywords: G protein-coupled receptor; transmembrane protein			
Query Match 37.6%; Score 667; DB 2; Length 314;			
Best Local Similarity 44.2%; Pred. No. 1.3e-49;			
Matches 129; Conservative 61; Mismatches 98; Indels 4; Gaps 2;			
QY	33	FVLLGFSARPSLETVLFIVVLSFYMVSIILGNIGIILVSHSTDVHLHTPMYFFLANLSFLDM	92
Db	12	FLLLFLPIPSEHQHFYALFLSMYLTTLGNLIIILIHLDShLHTPMYLFSLNLSFSDL	71
QY	93	SFTTSIVPQLLANLWGPQKTISYGGCVVQFYISHWLGATECVLLATMSYDRYAAICRPLH	152
Db	72	CFSSVTMPKLLQNMQSQVPSIPFAGCLTQLYFYLYFADLESFLLVAMAYDRYVAICFPLH	131
QY	153	YTVIMHPQLCLGLALASWLGLTT--SMVGSTLTMLPLCGNNCIDHFFCEMPLIMQLAC	210
Db	132	YMSIMSPKLCVSLVLSWV--LTTFHAMLHTLLMARLSFCADNMIPHFCDISPLLKLS	189
QY	211	VDTSLNEMMYLASFVFLPLGLILVSYGHIARAVLKIRSAEGRRAKAFNTCSSHVAVVS	270
Db	190	SDTHVNELVIFWVGGLVIVIPFVLIIVSYARVWASILKVPSVRGIHKIFSTCGSHLSVVS	249
QY	271	LFYGSIIIFMYLQPAKSTSHQGGKFIALFYTVVTPALNPLIYTLRNTEVKSAL	322
Db	250	LFYGTIIGLYLCPSSANNSTVKETVMAMMYTVVTPMLNPFYSLNRDMKEAL	301
RESULT 12			
S29710			
olfactory receptor OR18 - rat			
C:Species: Rattus norvegicus (Norway rat)			
C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998			
C:Accession: S29710			
R:Raming, K.; Krieger, J.; Strotmann, J.; Boekhoff, I.; Kubick, S.; Baumstark, C.; Bree			
Nature 361, 353-356, 1993			
A:Title: Cloning and expression of odorant receptors.			
A:Reference number: S29707; MUID:93149273; PMID:7678922			
A:Accession: S29710			
A:Molecule type: mRNA			
A:Residues: 1-307 <RAM>			
C:Superfamily: olfactory receptor OR14			
Query Match 37.4%; Score 665; DB 2; Length 307;			
Best Local Similarity 43.9%; Pred. No. 1.9e-49;			
Matches 134; Conservative 59; Mismatches 106; Indels 6; Gaps 3;			
QY	21	MMEIANVSSPEVFLLGFSARPSLETVLFIVVLSFYMVSIILGNIGIILVSHSTDVHLHTPM	80

Db	1	MGENNNITE--FILLGLTQDPDGRKALFVIFFLIYIVTMGNLLIVTVIASPSLGS	PM 57
QY	81	YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTISYGGCVQFYISHWLGATECVLLATMS	140
Db	58	YFFLASLSLLDALFSTAISPKLIADLLYDQKTISFRACMSQLFIEHLFGGVDIVILVAMA	117
QY	141	YDRYAAICRPLHYTVIMHPQLCLGLALASWLGLTTSVMVGSTLTMLPLCGNNCIDHFFC	200
Db	118	YDRYVAICKPLHYLAIMNRRVCITLLIFAWTGGFTHSLIQIVFVYNLPPFCGPNVIDHFIC	177
QY	201	EMPLIMQLACVDTSLNEMEMYLASFVFFVVLPLGLLILVSYGHIARAVLKIRSAEGRRAFN	260
Db	178	DMSPLLVLA	236
QY	261	TCSSHVAVVSLFYGSIIFMYLQPAKSTSHQGGKFIALFYTVVTPALNPLIYTLRNTEVKS	320
Db	237	TCSSHILVVILFFVPCIFMYARPVYNFPID--KCITVFYTIITPMLNPLIYTLRNSEIKS	294
QY	321	ALRHM	325
Db	295	CMKKL	299
RESULT 13			
E23701			
olfactory receptor I3 - rat			
C:Species: Rattus norvegicus (Norway rat)			
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004			
C:Accession: E23701			
R:Buck, L.; Axel, R.			
Cell 65, 175-187, 1991			
A:Title: A novel multigene family may encode odorant receptors: a molecular basis for od			
A:Reference number: A23701; MUID:91191556; PMID:1840504			
A:Accession: E23701			
A:Status: nucleic acid sequence not shown			
A:Molecule type: mRNA			
A:Residues: 1-310 <BUC>			
A:Cross-references: UNIPROT:P23269; GB:M64385; NID:g205831; PIDN:AAA41748.1; PID:g205832			
C:Superfamily: olfactory receptor OR14			
C:Keywords: G protein-coupled receptor; transmembrane protein			
Query Match 37.4%; Score 664; DB 2; Length 310;			
Best Local Similarity 44.6%; Pred. No. 2.4e-49;			
Matches 132; Conservative 61; Mismatches 99; Indels 4; Gaps 2;			
QY	33	FVLLGFSARPSLETVLFIVVLSFYMVSIILGNIGIILVSHSTDVHLHTPMYFFLANLSFLDM	92
Db	10	FLLLGLPIPEEHQHLFYALFLVMYLTTLGNLIIIVLVQLDSQLHTPMYLFSLNLSFSDL	69
QY	93	SFTTSIVPQLLANLWGPQKTISYGGCVVQFYISHWLGATECVLLATMSYDRYAAICRPLH	152
Db	70	CFSSVTMPKLLQNMRSDTISIPYGGCLAQTYFFMVFGDMESFLLVAMAYDRYVAICFPLH	129
QY	153	YTVIMHPQLCLGLALASWLGLTTS--MVGSTLTMLPLCGNNCIDHFFCEMPLIMQLAC	210
Db	130	YTSIMSPKLC	187
QY	211	VDTSLNEMMYLASFVFLPLGLILVSYGHIARAVLKIRSAEGRRAKAFNTCSSHVAVVS	270
Db	188	SDTYINELMIFIMSTLLIIIPFFFLIVMSYARIISSILKVPSTQGICKVFSTCGSHLSVVS	247
QY	271	LFYGSIIIFMYLQPAKSTSHQGGKFIALFYTVVTPALNPLIYTLRNTEVKSALRHMV	326
Db	248	LFYGTIIGLYLCPAGNNSTVKEMVMAMMYTVVTPMLNPFYSLNRDMKRALIRVI	303
RESULT 14			
S51356			
olfactory receptor - rat			
C:Species: Rattus norvegicus (Norway rat)			
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004			
C:Accession: S51356; S47014			
R:Gat, U.; Nekrasova, E.; Lancet, D.; Natochin, M.			

Eur. J. Biochem. 225, 1157-1168, 1994
A;Title: Olfactory receptor proteins. Expression, characterization and partial purification
A;Reference number: S51356; MUID:95045546; PMID:7957207
A;Accession: S51356
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-309 <GAT>
A;Cross-references: UNIPROT:Q63395; EMBL:X80671; NID:G517365; PIDN:CAA56697.1; PID:G517365
R;Gat, U.; Nekrasova, E.; Lancet, D.; Natochin, M.
submitted to the EMBL Data Library, July 1994
A;Description: Olfactory receptor proteins: expression, characterization and partial purification
A;Reference number: S47014
A;Accession: S47014
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-309 <GA2>
A;Cross-references: EMBL:X80671; NID:G517365; PIDN:CAA56697.1; PID:G517366
C;Superfamily: olfactory receptor OR14

Query Match 37.3%; Score 662; DB 1; Length 309;
Best Local Similarity 44.2%; Pred. No. 3.5e-49;
Matches 134; Conservative 67; Mismatches 100; Indels 2; Gaps 2;

QY	21	MMEIANVSSPEVFLGFSARPSLETVLFIIVLSFYMVSIILGN-GIIILVSHSTDVHLHTP	79
Db	1	MMGTGNHSAVVVFLVGLTKQPELLLPFLFLVIVYVLTVVGNLGMILLIIVSPL-LHTP	59
QY	80	MYFFLANLSFLDMSFTTSIVPQLLANLWGPQKTIISYGGCVVQFYISHWLGAECVLLATM	139
Db	60	MYIFLSSLSFVDLCYSTVITPRMLVNLFLGKNFITVSECMAQFFFAIFVVTGYYLLTVM	119
QY	140	SYDRYAAICRPLHYTVIMHPQCLGLALASWLGSLTSMVGSTLTMLPLCGNCCIDHFF	199
Db	120	AYDRYVAICRPLLYNVIMSSRICSLLVVAFSLGLFSAVVHTSAMNLSFCKSYIIISHYF	179
QY	200	CEPMLIMQLACVDTSLNEMEMVYLASFVVFVLPGLILVSYGHIAVARAVLKIRSAEGRRKAF	259
Db	180	CDALPLLKLACSNTHNELLIFFIGGLNTLVPTLVAISYVFFICSILRIRSEGRSKAF	239
QY	260	NTCSSHVAVVSLFYGSIIFMYLQPAKSTSHQKPIALFYTVVTPALNPLIYTLRNTEVK	319
Db	240	GTCSSHLMAVGIFFGSITFMYLKPSSNSLEQEKVSVFYTTVIPMLNPLIYSLRNKDVK	299
QY	320	SAL 322	
Db	300	KAL 302	

RESULT 15
C23701
olfactory receptor F6 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C;Accession: C23701
R;Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A;Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A;Reference number: A23701; MUID:91191556; PMID:1840504
A;Accession: C23701
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-311 <BUC>
A;Cross-references: UNIPROT:P23267; GB:M64378; NID:G205817; PIDN:AAA41741.1; PID:G205818
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 37.2%; Score 660; DB 2; Length 311;
Best Local Similarity 45.2%; Pred. No. 5.2e-49;
Matches 137; Conservative 53; Mismatches 109; Indels 4; Gaps 2;

QY	26	NVSSPEVFLGFSARPSLETVLFIIVLSFYMVSIILGNHIIILVSHSTDVH--LHTPMYFF	83
Db	8	NLSTPGPFILGFPGRSMRIGLFLFLVMYLLTVGN--LAIISLVGAHRCLOTPMYFF	65

QY	84	LANLSFLDMSFTTSIVPQLLANLWGPQKTIISYGGCVVQFYISHWLGAECVLLATMSYDR	143
Db	66	LCNLSFLEIWFETTACVPKTLATFAPRGGVISLAGCATQMYFVFSGLCTEYFLLAVMAYDR	125
QY	144	YAAICRPLHYTVIMHPQCLGLALASWLGSLTSMVGSTLTMLPLCGNCCIDHFFCEMP	203
Db	126	YLAICLPLRYGGIMTPGLAMRLALGSWLCGFSAITVPATLIARLSFCGSRVINHFFCDIS	185
QY	204	LIMQLACVDTSLNEMEMVYLASFVVFVLPGLILVSYGHIAVARAVLKIRSAEGRRKAFNTCS	263
Db	186	PWIVLSCTDQVVELVSFGIAFCVILGSCGITLVSYAYIIITTIKIPSARGHRAFSCTS	245
QY	264	SHVAVVSLFYGSIIFMYLQPAKSTSHQKPIALFYTVVTPALNPLIYTLRNTEVKSALR	323
Db	246	SHLTVVLIWYGSTIFLHVRTSVESLDTLKAITVLNTIVTPVLNPFYITLRNKDVKEALR	305
QY	324	HMV 326	
Db	306	RTV 308	

Search completed: April 8, 2005, 17:09:17
Job time : 47 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 17:05:35 ; Search time 140 Seconds
(without alignments)
806.279 Million cell updates/sec

Title: US-10-633-894-6
Perfect score: 1776
Sequence: 1 MPCMPCALPTGGLLPHPQHT.....ALRHMVLENC CGSAGKLAQI 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5:	/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6:	/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7:	/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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19:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1776	100.0	340	15	US-10-633-894-6
2	1767	99.5	340	9	US-09-886-055-465
3	1767	99.5	340	10	US-09-804-291-465
4	1725	97.1	377	15	US-10-343-650A-596
5	1651	93.0	320	11	US-09-981-566A-28
6	1646	92.7	320	15	US-10-005-041A-28
7	1645	92.6	320	14	US-10-017-161-566
8	1645	92.6	320	15	US-10-292-798-494
9	1640	92.3	319	16	US-10-473-518-39
10	1565	88.1	305	15	US-10-024-212-118
11	1009	56.8	317	17	US-10-774-355A-1895
12	990	55.7	350	9	US-09-886-055-397
13	990	55.7	350	10	US-09-804-291-397
					Sequence 6, Appli
					Sequence 465, App
					Sequence 465, App
					Sequence 596, App
					Sequence 28, Appl
					Sequence 28, Appl
					Sequence 566, App
					Sequence 494, App
					Sequence 39, Appl
					Sequence 118, App
					Sequence 1895, Ap
					Sequence 397, App
					Sequence 397, App

14	990	55.7	350	14	US-10-017-161-20	Sequence 20, Appl
15	990	55.7	350	15	US-10-343-650A-570	Sequence 570, App
16	985	55.5	312	10	US-09-795-271-58	Sequence 58, Appl
17	985	55.5	312	10	US-09-907-218-47	Sequence 47, Appl
18	985	55.5	312	10	US-09-907-218-78	Sequence 78, Appl
19	985	55.5	312	10	US-09-912-976-55	Sequence 55, Appl
20	985	55.5	312	10	US-09-912-976-61	Sequence 61, Appl
21	985	55.5	312	10	US-09-965-422-49	Sequence 49, Appl
22	985	55.5	312	11	US-09-981-566A-29	Sequence 29, Appl
23	985	55.5	312	15	US-10-005-041A-95	Sequence 95, Appl
24	985	55.5	312	15	US-10-005-041A-107	Sequence 107, App
25	985	55.5	334	10	US-09-965-422-10	Sequence 10, Appl
26	984.5	55.4	309	10	US-09-912-976-16	Sequence 16, Appl
27	984.5	55.4	309	10	US-09-965-422-12	Sequence 12, Appl
28	984.5	55.4	309	14	US-10-032-189-111	Sequence 111, App
29	984.5	55.4	309	15	US-10-292-798-18	Sequence 18, Appl
30	984.5	55.4	309	16	US-10-467-252-32	Sequence 32, Appl
31	984	55.4	312	10	US-09-795-271-12	Sequence 12, Appl
32	984	55.4	334	9	US-09-886-055-365	Sequence 365, App
33	984	55.4	334	10	US-09-804-291-365	Sequence 365, App
34	983	55.3	312	17	US-10-774-355A-1915	Sequence 1915, Ap
35	981	55.2	315	10	US-09-912-976-20	Sequence 20, Appl
36	978	55.1	334	10	US-09-965-422-4	Sequence 4, Appli
37	978	55.1	334	15	US-10-005-041A-32	Sequence 32, Appl
38	977.5	55.0	309	10	US-09-912-976-18	Sequence 18, Appl
39	977	55.0	314	17	US-10-774-355A-1902	Sequence 1902, Ap
40	977	55.0	334	10	US-09-965-422-6	Sequence 6, Appli
41	977	55.0	334	10	US-09-965-422-8	Sequence 8, Appli
42	977	55.0	334	15	US-10-633-894-8	Sequence 8, Appli
43	976	55.0	311	10	US-09-795-271-62	Sequence 62, Appl
44	976	55.0	312	10	US-09-795-271-55	Sequence 55, Appl
45	976	55.0	312	11	US-09-981-566A-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-10-633-894-6
; Sequence 6, Application US/10633894
; Publication No. US20040029232A1
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Yang, Jianxin
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20040029232A1el G-Protein Coupled Receptors
; FILE REFERENCE: 018781-004720US
; CURRENT APPLICATION NUMBER: US/10/633,894
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US/09/546,986A
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 09/524,730
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-633-894-6

Query Match 100.0%; Score 1776; DB 15; Length 340;
Best Local Similarity 100.0%; Pred. No. 1.5e-156;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MPCMPCALPTGGLLPHPQHTMMEIANVSSPEVFLGFSARPSLETVLFI	VLSFYMVSI	60
Db	1	MPCMPCALPTGGLLPHPQHTMMEIANVSSPEVFLGFSARPSLETVLFI	VLSFYMVSI	60
Qy	61	LGNGIIILVSHTDVHLHTPMYFFFLANLSFLDMSFTTSIVPQLLANLWGPQK	TSYGGCW	120
Db	61	LGNGIIILVSHTDVHLHTPMYFFFLANLSFLDMSFTTSIVPQLLANLWGPQK	TSYGGCW	120

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Db 121 QFYISHWLGATECVLLATMSYDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSMSG 180
QY 181 STLTMLLPLCGNNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFWVPLPLGLILVSYG 240
Db 181 STLTMLLPLCGNNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFWVPLPLGLILVSYG 240
QY 241 HIARAVLKIRSAEGRKAFNTCSSHVAVVSFLFYGSIIFMYLQPAKSTSHEQGKFIALFYT 300
Db 241 HIARAVLKIRSAEGRKAFNTCSSHVAVVSFLFYGSIIFMYLQPAKSTSHEQGKFIALFYT 300
QY 301 VVTPALNPLIYTLRNTTEVKSALRHMVLENCSSAGKLAQI 340
Db 301 VVTPALNPLIYTLRNTTEVKSALRHMVLENCSSAGKLAQI 340

RESULT 2

US-09-886-055-465
; Sequence 465, Application US/09886055
; Patent No. US20020132273A1
; GENERAL INFORMATION:
; APPLICANT: STRYER, LUBERT
; APPLICANT: ZOZULA, SERGEY
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
; TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
; FILE REFERENCE: 078003-0277150
; CURRENT APPLICATION NUMBER: US/09/886,055
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,812
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 522
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 465
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-886-055-465

Query Match 99.5%; Score 1767; DB 9; Length 340;
Best Local Similarity 99.4%; Pred. No. 1e-155;
Matches 338; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPCMPCALPTGGLPHQHTMMEIANVSSPEVFLGFSARPSLETVLFIVVLSFYMVSI 60
Db 1 MPCMPCALPTGGLPHQHTMMEIANVSSPEVFLGFSARPSLETVLFIVVLSFYMVSI 60
QY 61 LGNGIILVSHTDVHLHTPMYFFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSYGGCVV 120
Db 61 LGNGIILVSHTDVHLHTPMYFFFLANLPFLDMSFTTSIVPQLLANLWGPQKTSYGGCVV 120
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Db 121 QFYISHWLGATECVLLATMSYDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSMSG 180
QY 181 STLTMLLPLCGNNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFWVPLPLGLILVSYG 240
Db 181 STLTMLLPLCGNNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFWVPLPLGLILVSYG 240
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Db 241 HIARAVLKIRSAEGRKAFNTCSSHVAVVSFLFYGSIIFMYLQPAKSTSHEQGKFIALFYT 300
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Db 301 VVTPALNPLIYTLRNTTEVKSALRHMVLENCSSAGKLAQI 340

RESULT 3

US-09-804-291-465
; Sequence 465, Application US/09804291
; Publication No. US2003008059A1

; GENERAL INFORMATION:
; APPLICANT: ZOZULA, SERGEY
; TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: P 0278005
; CURRENT APPLICATION NUMBER: US/09/804,291
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/188,914
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/192,033
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/198,474
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/199,335
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 60/207,702
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/213,849
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/226,534
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/230,732
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/266,862
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 465
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-804-291-465

Query Match 99.5%; Score 1767; DB 10; Length 340;
Best Local Similarity 99.4%; Pred. No. 1e-155;
Matches 338; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 61 LGNGIILVSHTDVHLHTPMYFFFLANLPFLDMSFTTSIVPQLLANLWGPQKTSYGGCVV 120
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Db 121 QFYISHWLGATECVLLATMSYDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSMSG 180
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Db 181 STLTMLLPLCGNNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFWVPLPLGLILVSYG 240
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Db 241 HIARAVLKIRSAEGRKAFNTCSSHVAVVSFLFYGSIIFMYLQPAKSTSHEQGKFIALFYT 300
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Db 301 VVTPALNPLIYTLRNTTEVKSALRHMVLENCSSAGKLAQI 340

RESULT 4

US-10-343-650A-596
; Sequence 596, Application US/10343650A
; Publication No. US20040067499A1
; GENERAL INFORMATION:
; APPLICANT: HAGA, TATSUYA
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 31671-186347
; CURRENT APPLICATION NUMBER: US/10/343,650A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000/237818
; PRIOR FILING DATE: 2000-08-04

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; PRIOR APPLICATION NUMBER: JP 2001/34434
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 596
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (10)..(43)
; OTHER INFORMATION: Variable amino acid
US-10-343-650A-596

Query Match      97.1%; Score 1725; DB 15; Length 377;
Best Local Similarity 99.4%; Pred. No. 9.4e-152;
Matches 332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY  67  ILVSHTDVHLHTPMYFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSISGGCVVQFYISH 126
Db  104 ILVSHTDVHLHTPMYFFLANLPFLDMSFTTSIVPQLLANLWGPQKTSISGGCVVQFYISH 163

QY  127 WLGATECVLLATMSYDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTSMVGSTLTML 186
Db  164 WLGATECVLLATMSYDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTSMVGSTLTML 223

QY  187 LPLCGNNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFFVPLPLGLILVSYGHIARAV 246
Db  224 LPLCGNNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFFVPLPLGLILVSYGHIARAV 283

QY  247 LKIRSAEGRRKAFNTCSSHVAVVSLFYGSIIFMYLQPAKSTSHQCKFIALFYTVVTPAL 306
Db  284 LKIRSAEGRRKAFNTCSSHVAVVSLFYGSIIFMYLQPAKSTSHQCKFIALFYTVVTPAL 343

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Db  344 NPLIYTLRNTVEKSA LRHMVLENC CGSAGKLAQI 377
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RESULT 5
US-09-981-566A-28
; Sequence 28, Application US/09981566A
; Publication No. US20040005656A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda et al.
; TITLE OF INVENTION: No. US20040005656A1el GPCR-like Proteins and Nucleic Acids Encodi
; TITLE OF INVENTION: Same
; FILE REFERENCE: 21402-163
; CURRENT APPLICATION NUMBER: US/09/981,566A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/240,704
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/262,159
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/263,340
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/264,118
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/308,203
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/243,497
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/244,542
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: 60/269,031
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/245,484
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: 60/255,017
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; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/263,216
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/268,225
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 209
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-981-566A-28

Query Match      93.0%; Score 1651; DB 11; Length 320;
Best Local Similarity 99.7%; Pred. No. 5.8e-145;
Matches 319; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  21  MMEIANVSSPEVFLGFSARPSLETVLFIVVLSFYMVSIILNGIILVSHTDVHLHTPM 80
Db  1  MMEIANVSSPEVFLGFSARPSLETVLFIVVLSFYMVSIILNGIILVSHTDVHLHTPM 60

QY  81  YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSISGGCVVQFYISHWLGATECVLLATMS 140
Db  61  YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSISGGCVVQFYISHWLGATECVLLATMS 120

QY  141 YDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTSMVGSTLTMLPLCGNNCIDHFFC 200
Db  121 YDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTSMVGSTLTMLPLCGNNCIDHFFC 180

QY  201 EMPLIMQLACVDTSLNEMEMYLASFVFFVPLPLGLILVSYGHIARAVLKIRSAEGRRKAFN 260
Db  181 EMPLIMQLACVDTSLNEMEMYLASFVFFVPLPLGLILVSYGHIARAVLKIRSAEGRRKAFN 240

QY  261 TCSSHVAVVSLFYGSIIFMYLQPAKSTSHQCKFIALFYTVVTPALNPVIYTLRNTVEKS 320
Db  241 TCSSHVAVVSLFYGSIIFMYLQPAKSTSHQCKFIALFYTVVTPALNPVIYTLRNTVEKS 300

QY  321 ALRHMVLENC CGSAGKLAQI 340
Db  301 ALRHMVLENC CGSAGKLAQI 320
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RESULT 6
US-10-005-041A-28
; Sequence 28, Application US/10005041A
; Publication No. US2003023231A1
; GENERAL INFORMATION:
; APPLICANT: Casman, Stacie J
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shimkets, Richard A
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Gilbert, Jennifer A
; APPLICANT: Mayotte, Jane E
; APPLICANT: Baumgartner, Jason C
; APPLICANT: Mishra, Vishnu
; APPLICANT: Vernet, Corine AM
; APPLICANT: Dickinson, Kevin S
; APPLICANT: Ballinger, Robert A
; APPLICANT: Wolenc, Adam R
; APPLICANT: Edinger, Shlomit R
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glennnda
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Gerlach, Valerie
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-215
; CURRENT APPLICATION NUMBER: US/10/005,041A
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/251,459
; PRIOR FILING DATE: 2000-12-05
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; PRIOR APPLICATION NUMBER: 60/259,007
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-005-041A-28

Query Match      92.7%;   Score 1646;   DB 15;   Length 320;
Best Local Similarity 99.4%;   Pred. No. 1.7e-144;
Matches 318;   Conservative 1;   Mismatches 1;   Indels 0;   Gaps 0;

QY      21 MMEIANVSSPEVFLVLLGFSARPSLETVLFIIVLSFYMVSIILGNGIILVSHSTDVHLHTPM 80
Db      1 MMEIANVSSPEVFLVLLGFSARPSLETVLFIIVLSFYMVSIILGNGIILVSHSTDVHLHTPM 60

QY      81 YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSISYGGCVVQFYISHWLGATECVLLATMS 140
Db      61 YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSISYGGCVVQFYISHWLGATECVLLATMS 120

QY      141 YDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVMGSTLTMLPLCGNNCIDHFFC 200
Db      121 YDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVMGSTLTMLPLCGNNCIDHFFC 180

QY      201 EMPLIMQLACVDTSLNEMEMYLASFVFWVPLPLGLILVSYGHIARAVLKIRSAEGRRKAFN 260
Db      181 EMPLIMQLACVDTSLNEMEMYLASFVFWVPLPLGLILVSYGHIARAVLKIRSAEGRRKAFN 240

QY      261 TCSSSHVAVVSLFYGSIIFMYLQPAKSTSHEQGFIALFYTVVTPALNPLIYTLRNTEVKS 320
Db      241 TCSSSHVAVVSLFYGSIIFMYLQPAKSTSHEQGFIALFYTVVTPALNPNVIYTLRNTEVKS 300

QY      321 ALRHMVLECCGSAGKLAQI 340
Db      301 ALRHMVLECCGSAGKLAQI 320

RESULT 7
US-10-017-161-566
; Sequence 566, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 566
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-566

Query Match      92.6%;   Score 1645;   DB 14;   Length 320;
Best Local Similarity 99.4%;   Pred. No. 2.1e-144;
Matches 318;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

QY      21 MMEIANVSSPEVFLVLLGFSARPSLETVLFIIVLSFYMVSIILGNGIILVSHSTDVHLHTPM 80
Db      1 MMEIANVSSPEVFLVLLGFSARPSLETVLFIIVLSFYMVSIILGNGIILVSHSTDVHLHTPM 60

QY      81 YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSISYGGCVVQFYISHWLGATECVLLATMS 140
Db      61 YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSISYGGCVVQFYISHWLGATECVLLATMS 120

QY      141 YDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVMGSTLTMLPLCGNNCIDHFFC 200
Db      121 YDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVMGSTLTMLPLCGNNCIDHFFC 180

QY      201 EMPLIMQLACVDTSLNEMEMYLASFVFWVPLPLGLILVSYGHIARAVLKIRSAEGRRKAFN 260
Db      181 EMPLIMQLACVDTSLNEMEMYLASFVFWVPLPLGLILVSYGHIARAVLKIRSAEGRRKAFN 240

QY      261 TCSSSHVAVVSLFYGSIIFMYLQPAKSTSHEQGFIALFYTVVTPALNPLIYTLRNTEVKS 320
Db      241 TCSSSHVAVVSLFYGSIIFMYLQPAKSTSHEQGFIALFYTVVTPALNPNVIYTLRNTEVKS 300

RESULT 8
US-10-292-798-494
; Sequence 494, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 494
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-494

Query Match      92.6%;   Score 1645;   DB 15;   Length 320;
Best Local Similarity 99.4%;   Pred. No. 2.1e-144;
Matches 318;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

QY      21 MMEIANVSSPEVFLVLLGFSARPSLETVLFIIVLSFYMVSIILGNGIILVSHSTDVHLHTPM 80
Db      1 MMEIANVSSPEVFLVLLGFSARPSLETVLFIIVLSFYMVSIILGNGIILVSHSTDVHLHTPM 60

QY      81 YFFLANLSFLDMSFTTSIVPQLLANLWGPQKTSISYGGCVVQFYISHWLGATECVLLATMS 140
Db      61 YFFLANLPFLDMSFTTSIVPQLLANLWGPQKTSISYGGCVVQFYISHWLGATECVLLATMS 120

QY      141 YDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVMGSTLTMLPLCGNNCIDHFFC 200
Db      121 YDRYAAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVMGSTLTMLPLCGNNCIDHFFC 180

QY      201 EMPLIMQLACVDTSLNEMEMYLASFVFWVPLPLGLILVSYGHIARAVLKIRSAEGRRKAFN 260
Db      181 EMPLIMQLACVDTSLNEMEMYLASFVFWVPLPLGLILVSYGHIARAVLKIRSAEGRRKAFN 240

QY      261 TCSSSHVAVVSLFYGSIIFMYLQPAKSTSHEQGFIALFYTVVTPALNPLIYTLRNTEVKS 320
Db      241 TCSSSHVAVVSLFYGSIIFMYLQPAKSTSHEQGFIALFYTVVTPALNPNVIYTLRNTEVKS 300

QY      321 ALRHMVLECCGSAGKLAQI 340
Db      301 ALRHMVLECCGSAGKLAQI 320

RESULT 9
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Db 195 ASSLIHATFTLQLPLCGNHRLDHFICEVPALLKLACVDTTVNELVLFVVSVLFVVIPPAL 254
QY 235 ILVSYGHIARAVLKIRSAEGRRKAENTCSSHVAVVSLFYGSIIIFYLQPAKSTSHQGGKF 294
Db 255 ISISYGFITQAVLRIKSVEARHKAFSTCSSHLTVVIFYGTIIYVYLQPSDSYAQDQGGKF 314
QY 295 IALFYTVVTPALNPLIYTLRNTTEVKSALRHMVLENC CGSAGKL 337
Db 315 ISLFYTMVTPTLNPIIYTLRNKDMKEALRKLL-----SGKL 350

Search completed: April 8, 2005, 17:15:42
Job time : 142 secs